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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

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DESCRIPTION
PROTEIN KINASES

FIELD OF THE INVENTION

5 The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10 The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

 Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key
15 biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

 Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:
20 cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the
25 etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

 The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism
30 includes changes in the catalytic properties (V_{max} and K_m) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple alignment of the sequences in the catalytic domain of protein kinases and subsequent
20 parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

25 We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

30 Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungus-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5 The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

10 The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca²⁺/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

15 CMGC group kinases are "proline-directed" enzymes phosphorylating residues that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

20 The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

25 Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close
30 homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD_sp, YGR262_sc) kinases, and others that are "unique" and don't cluster into any obvious family.

SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
5 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides
conjugated to each other, including DNA and RNA, that is isolated from a natural source
10 or that is synthesized. The isolated nucleic acid of the present invention is unique in the
sense that it is not found in a pure or separated state in nature. Use of the term "isolated"
indicates that a naturally occurring sequence has been removed from its normal cellular
(*i.e.*, chromosomal) environment. Thus, the sequence may be in a cell-free solution or
placed in a different cellular environment. The term does not imply that the sequence is
15 the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at
least) of non-nucleotide material naturally associated with it, and thus is distinguished
from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the
specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of
20 the total DNA or RNA present in the cells or solution of interest than in normal or
diseased cells or in the cells from which the sequence was taken. This could be caused by
a person by preferential reduction in the amount of other DNA or RNA present, or by a
preferential increase in the amount of the specific DNA or RNA sequence, or by a
combination of the two. However, it should be noted that enriched does not imply that
25 there are no other DNA or RNA sequences present, just that the relative amount of the
sequence of interest has been significantly increased. The term "significant" is used to
indicate that the level of increase is useful to the person making such an increase, and
generally means an increase relative to other nucleic acids of about at least 2 fold, more
preferably at least 5 to 10 fold or even more. The term also does not imply that there is no
30 DNA or RNA from other sources. The other source DNA may, for example, comprise
DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term
distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6 -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

5 SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
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SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
10 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional
15 derivatives thereof as described herein. For sequences for which the full-length sequence
is not given, the remaining sequences can be determined using methods well-known to
those in the art and are intended to be included in the invention. In certain aspects,
polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide
can be encoded by a full-length nucleic acid sequence or any portion of the full-length
20 nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By
“functional” domain is meant any region of the polypeptide that may play a regulatory or
catalytic role as predicted from amino acid sequence homology to other proteins or by the
presence of amino acid sequences that may give rise to specific structural conformations
(*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but
25 not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from
the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
30 NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID
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NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding
20 full-length amino acid sequence, or fragments thereof. A sequence that is substantially
similar to a sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
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By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402), Blast2 (Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) *J. Mol. Biol.* 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

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NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID
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NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will
15 have at least 75% identity (preferably 90%, more preferably at least 95% and most
preferably 99-100%) to the sequence selected from the group consisting of those set forth
in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
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NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
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5 NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
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NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c)
10 hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes
a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an
amino acid sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
15 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
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NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
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NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
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30 NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
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5 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
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NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
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15 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
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NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
25 ID NO:242, except that it lacks one or more, but not all, of a domain selected from the
group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a
coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-
terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a
polypeptide having an amino acid sequence selected from the group consisting of those set
30 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

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NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, 5 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, 10 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, 15 SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, 20 SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, 25 SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, 30 a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

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SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at
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100%) to the sequence selected from the group consisting of those set forth in SEQ ID
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NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
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NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
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NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
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occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
20 NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
25 NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
30 NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID

NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) *J. Biol. Chem.* 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further,
10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate
20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine
25 amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of
30 the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

domain may play a regulatory role is PAK3 which contains a heterotrimeric G_i subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic α -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein-protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).
5 Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of
10 the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein
15 database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these
20 methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the
25 protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of
30 the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4 , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

5 The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding
10 a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

 The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field,
15 detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

 The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes,
20 the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

25 In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19,
30 SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
5 NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
15 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.
25 In particular, a unique nucleic acid region is preferably of mammalian origin and
preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of
nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is
selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe
contains a nucleotide base sequence that will hybridize to a sequence selected from the
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the
genomic regulatory elements, or may be under the control of exogenous regulatory
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence. By "fragment," is meant an amino acid sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
5 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-
length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase
polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ
10 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ
15 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
20 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
25 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
30 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (*e.g.*, in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5 In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
10 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
15 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
20 SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
25 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
30 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242 where the domain is selected from the group consisting of an N-terminal domain,
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
5 SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it
lacks one or more, but not all, of the domains selected from the group consisting of a C-
terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich
10 region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain
demarcations of the polypeptides of the invention are indicated in Table 2 by reference to
the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in
the art. The natural source may be mammalian, preferably human, blood, semen, or tissue,
15 and the polypeptide may be synthesized using an automated polypeptide synthesizer. The
isolated, enriched, or purified kinase polypeptide is preferably selected from the group
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
20 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ
25 ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ
30 ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ
ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

10 In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, 15 SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, 20 SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, 25 SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, 30 SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By "recombinant kinase polypeptide" is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By "specific binding affinity" is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term "specific binding affinity" describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term "polyclonal" refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

"Monoclonal antibodies" are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term "antibody fragment" refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
5 NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID
NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID
10 NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and
where the domains are defined as above. By "hybridoma" is meant an immortalized cell
15 line that is capable of secreting an antibody, for example an antibody to a kinase of the
invention. In preferred embodiments, the antibody to the kinase comprises a sequence of
amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able
to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122,
20 SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,
25 SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,
SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,
SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
30 SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242. The binding agent is preferably a purified antibody that recognizes an epitope
present on a kinase polypeptide of the invention. Other binding agents include molecules
that bind to kinase polypeptides and analogous molecules that bind to a kinase
15 polypeptide. Such binding agents may be identified by using assays that measure kinase
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a
kinase polypeptide of the invention or an equivalent sequence. The method involves
identifying the novel polypeptide in human cells using techniques that are routine and
20 standard in the art, such as those described herein for identifying the kinases of the
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)
measuring the activity of said polypeptide; and (c) determining whether said substance
modulates the activity of said polypeptide.

20 The term “modulates” refers to the ability of a compound to alter the function of a
kinase of the invention. A modulator preferably activates or inhibits the activity of a
kinase of the invention.

 The term “activates” refers to increasing the cellular activity of the kinase. The
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is
25 preferably the interaction with a natural binding partner.

 The term “modulates” also refers to altering the function of kinases of the
invention by increasing or decreasing the probability that a complex forms between the
kinase and a natural binding partner. A modulator preferably increases the probability that
such a complex forms between the kinase and the natural binding partner, more preferably
30 increases or decreases the probability that a complex forms between the kinase and the
natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term "complex" refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules
5 bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term "natural binding partner" refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase
10 and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term "contacting" as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution
15 comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

20 In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of
SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126,
SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131,
25 SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,
30 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
10 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
15 and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change
in cell phenotype or the interaction between said polypeptide and a natural binding
partner.

The term "expressing" as used herein refers to the production of kinases of the
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic
20 acid vector is transfected into cells using well known techniques in the art as described
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal
condition by administering to a patient in need of such treatment a substance that
modulates the activity of a polypeptide selected from the group consisting of SEQ ID
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, arteriosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, arteriosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term "preventing" refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5 The term "treating" refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

 The term "therapeutic effect" refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of
10 abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating
15 efficacy against abnormal conditions can be identified as described herein.

 The term "abnormal condition" refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in
20 normal cell cycle progression through mitosis and meiosis.

 Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

25 Abnormal differentiation conditions include, but are not limited to neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

 Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the
30 protein kinases could lead to cell immortality or premature cell death.

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

5 ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
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ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
10 ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
15 ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe
comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the
complements of the sequences and fragments; and (b) detecting the presence or amount of
20 the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from
the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, organ
transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative
stress-related neurodegenerative disorders, metabolic disorder including diabetes,
25 reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group
consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID
NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ
ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID
30 NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20,
SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36,
SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ
ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID
NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52,
5 SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ
ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID
NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68,
SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ
ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID
10 NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84,
SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ
ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID
NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID
NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID
15 NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID
NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID
NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID
NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional
derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically
20 hybridize. Specific hybridization indicates that in the presence of other nucleic acids the
probe only hybridizes detectably with the kinase of the invention's target region. Putative
target regions can be identified by methods well known in the art consisting of alignment
and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target
25 region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous
amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID
30 NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

5 NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID
NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID
10 NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID
NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID
15 NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding
full-length amino acid sequence, or a functional derivative thereof. Hybridization
20 conditions should be such that hybridization occurs only with the kinase genes in the
presence of other nucleic acid molecules. Under stringent hybridization conditions only
highly complementary nucleic acid sequences hybridize. Preferably, such conditions
prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20
contiguous nucleotides. Such conditions are defined *supra*.

25 Hybridization conditions should be such that hybridization occurs only with the
genes in the presence of other nucleic acid molecules. Under stringent hybridization
conditions only highly complementary nucleic acid sequences hybridize. Preferably, such
conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20
contiguous nucleotides. Such conditions are defined *supra*.

30 The diseases for which detection of kinase genes in a sample could be diagnostic
include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in
comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

"Amplification" as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker et al., EPO Publication No. 0 520 722
10 A1; Jones et al., U.S. Patent No. 4,447,608; Kabbe et al., U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5,316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker et al., Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin et al., Br. J. Cancer 53:361-368 (1986); Fernandes et al., Cancer Research 43:1117-1123 (1983); Ferris et al. J. Org. Chem. 44(2):173-178; Fry et al., Science 265:1093-1095 (1994); Jackman et al., Cancer Research 51:5579-5586 (1981); Jones et al. J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus et al., J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell et al.,
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini et al., Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece et al., Cancer Research 47(11):2996-2999 (1977); Sculier et al., Cancer Immunol. and Immunother. 23:A65 (1986); Sikora et al., Cancer Letters 23:289-295 (1984); and Sikora et al., Analytical Biochem. 172:344-355 (1988), all of which are incorporated
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle et al., J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke et al., J. Med. Chem. 36:425-432
30 (1993); and Burke et al. BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental
5 Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., " J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer
Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992);
10 Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular
Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J.
Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol.
15 Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996,
20 incorporated herein by reference in its entirety, including any drawings.
Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number
25 WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being
30 treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

5 Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the
10 screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:
15 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is
20 present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).
25 Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse
30 effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting
5 differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include,
10 but are not limited to, those discussed previously.

The term "comparing" as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine
15 these discrepancies in sequences are well-known to one of ordinary skill in the art. The "control" nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the
20 narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred
25 embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34,
SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ
ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID
NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50,
5 SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ
ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID
NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66,
SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ
ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID
10 NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82,
SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ
ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID
NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98,
SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103,
15 SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108,
SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113,
SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,
SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

20 DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding
such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides,
assays utilizing such polypeptides, and methods relating to all of the foregoing. The
present invention is based upon the isolation and characterization of new kinase
25 polypeptides. The polypeptides and nucleic acids may be produced using well-known and
standard synthesis techniques when given the sequences presented herein.

I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the
30 herein-described isolated nucleic acid molecules. The degeneracy of the genetic code
permits substitution of certain codons by other codons that specify the same amino acid
and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13,
SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ
ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID
NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29,
5 SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ
ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID
NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45,
SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ
ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID
10 NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61,
SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ
ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID
NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77,
SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ
15 ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID
NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93,
SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ
ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID
NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID
20 NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID
NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide
or polynucleotide may be used in this regard, provided that its addition, deletion or
substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123,
25 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
30 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded
by the nucleotide sequence. For example, the present invention is intended to include any
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or
its derivative. Moreover, the nucleic acid molecule of the present invention may, as
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity
25 to promote secretion and/or processing of heterologous proteins encoded by foreign
nucleic acid sequences fused thereto, for example. All variations of the nucleotide
sequence of the kinase genes of the invention and fragments thereof permitted by the
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with
30 codons other than degenerate codons to produce a structurally modified polypeptide, but
one which has substantially the same utility or activity as the polypeptide produced by the
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5 Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.
10 Therefore, these nucleic acid molecules are also part of the invention.

 The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore
15 presumably define new protein kinase groups.

 Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

20 II. Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

 A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,
25 Sambrook, Fritsch, & Maniatis, eds., 1989).

 In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain
30 reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

5 A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the
10 regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of
15 transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and
20 polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence
25 encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the
30 promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells.

5 Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

10 In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include γ gt10, γ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

15 Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

20 To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ , the *bla* promoter of the β -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the α -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ζ -28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

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promoters are reviewed by Glick (Ind. Microbiot. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

5 Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells"

10 include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention

15 are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid

20 origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and

25 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987;

30 Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184, π VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kiado, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
 SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
 SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
 5 SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
 SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
 SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
 10 SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
 NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of
 these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-
 15 terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are
 provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI,
 CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant
 number of protein kinases that do not belong to any of the known groups, and therefore
 20 presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1,
 Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein 25 Kinases

The present invention relates to an antibody having binding affinity to a kinase of
 the invention. The polypeptide may have an amino acid sequence selected from the group
 consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
 ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
 30 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
 ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

5 ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ
ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ
ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ
10 ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ
ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ
ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ
ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ
15 ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ
ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ
ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ
ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ
ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ
20 ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or
at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more
contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the
polypeptide not provided in the sequences above, but that is present in the full-length
sequence of the polypeptide and that is easily obtained using methods standard in the art.
25 Further, the antibody may bind specifically to particular domains of one or more of the
kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or
C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to
a kinase or kinase domain of the invention. Such an antibody may be isolated by
30 comparing its binding affinity to a kinase of the invention with its binding affinity to other
polypeptides. Those that bind selectively to a kinase of the invention would be chosen for
use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

5 The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

10 The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

15 The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

20 In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

25 The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

30

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Agl4 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed anti-peptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S.
20 Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune, neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatin, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

5 Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

 Tumor associated: Mok (SEQ ID NO:NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

 Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

15 Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

 Neuronal restricted: CAMKKB (SEQ ID NO:66)

 Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

20 Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

 Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

VIII. Transgenic Animals.

 A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (*e.g.*, the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (*Experientia* 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO₂ asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, *Cell* 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

5 In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous
10 kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

15 Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot
20 function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding
25 recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley
30 Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is
10 precipitated with CaPO_4 and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic acid molecule into a cell. Gene transfer is commonly performed to enable the expression
25 of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express
5 a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid
10 sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or
15 modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

20 X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by
25 reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of
30 the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

15 EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases
Materials and Methods Identification from cDNA databases and isolation of clones
encoding novel protein kinases

Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ m TESK2_m	GCTGCTGGACAGTGACT TGTATTT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAACT GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATT TGAAAAT	CTTCATCATCTCTAATACAT TGGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 - Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

10

Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

15

PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flt	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

5

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

10

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The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the evc (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

5 Human 5R79-46-1_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- κ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

15 Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

20 Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceded by the sequence "RGLLAPGDPPCPPNPAPATPPSSRLPTLFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

30 Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

5 Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

10 Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102
15 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

20 Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

25 Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

30 Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324_h orthologue of W30246_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP_057440) used for the Smith-Waterman query): N-term from Incyte 6010175_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175_2, Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to
15 encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

5 Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015_m (SEQ ID NO: 42, SEQ ID NO:162)

tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

15 The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

20 Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5 Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10 Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15 Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20 Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

25 Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478_m (SEQ ID NO:80, SEQ ID NO:199)

Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSNGEHGHGMNPSLQAMMLMGFGDI
FSMKNKAGAVMHSGMQINMQAKQNSS

KTTSKRRGKKVNMALGFSDFDLSEGDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

5 Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

10 Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

15 Human SGK022 orthologue of AA060026_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

20 Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

25 Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP_h 6921333_9; removed intron (146-893) predicted from blastx analysis.

30

Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG_040010.

Human orthologue of AA671275_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

5 The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

10 The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

78	92
79	93
80	94
157	193

Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASStar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca ²⁺ /calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

SGK	Serum and glucocorticoid-regulated kinase
STK	serine threonine kinase
ULK	UNC-51-like kinase

The following abbreviations were used for species

H	Human
M	Murine
R	Rat
FV	Fowlpox virus
MT	<i>M. thermoautotrophicum</i>
CE	<i>Caenorhabditis elegans</i>
DM	<i>Drosophila melanogaster</i>
OS	<i>Oryza sativa</i>
SP	<i>Schizosaccharomyces pombe</i>
TP	<i>Tetrahymena pyriformis</i>
PI	<i>Petunia inflata</i>
NC	<i>Neurospora crassa</i>
MSV	<i>Medicago sativa</i>
MSV	Moloney murine sarcoma virus
SA	<i>Squalus acanthias</i>
CS	<i>Cucumis sativus</i>
GM	<i>Glycine max</i>
LL	<i>Lilium longiflorum</i>
TV	<i>Trichomonas vaginalis</i>
MP	<i>Mycoplasma pneumoniae</i>
DD	<i>Dictyostelium discoideum</i>
SC	<i>Saccharomyces cerevisiae</i>
MT	<i>Methanobacterium thermoautotrophicum</i>

Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program (www.ch.embnet.org/software/COILS_form.html). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind (www.at.embnet.org/embnet/tools/bio/PESTfind/). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

Identification of potential coiled-coil domains and PEST domains in N34132

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coiled-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

5 Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

10 EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map (http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query
5 against databases, such as dbsts and htgs (described at http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above,
10 Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the
15 entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline
20 (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

Results

25 The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with
30 chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

EXAMPLE 3: Generation of Specific Immunoreagents

5 Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

10 Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLKRSQDLPRELP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRLD	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYYYKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDERDEEAVK	375-388
		SPGQGKDHKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPFDWEKTGNDGSLT	293-307
		HRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRS	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VDSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDREVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDEEDWGS	637-651
		SVSEDPTQLEEVKED	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein KinasesGENE EXPRESSION ANALYSIS

Tissue Arrays

“cDNA libraries” derived from a variety of sources were immobilized onto nylon
5 membranes and probed with 32P-labeled cDNA fragments derived from the gene(s) of
interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to
generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at
each end. An oligo dT primer containing a specific sequence (CDS:
10 AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at
the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV
RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when
it adds additional C residues. If a primer (SMII:
AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G:
15 AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals
to the added Cs and the MMLV recognizes the rest of the primer sequence as template and
continues transcription. As a result, the synthesized cDNAs contain specific sequence tags
at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same
sequence (CDS and SMII) it is referred to as “symmetric.” When the 5' end is tagged
20 with a different sequence than the 3' end (CDS and ML2G) is referred to as “asymmetric”
A double-stranded “cDNA library “ is then generated by PCR amplification using the
3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2:
AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified “cDNA libraries” were manually arrayed onto nylon membranes
25 with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and
cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech)
and hybridized with 32P labeled probes generated by random hexamer priming of cDNA
fragments corresponding to the genes of interest. After washing, the blots were exposed to
phosphorimaging cassettes and the intensity of the signal was quantified. The amount of
30 the DNA on the arrays was also quantified by treating non-denatured or denatured arrays
with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2
minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

5 Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AI086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

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EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

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Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

20 EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Db1 and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

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Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ
5 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ
10 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
15 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
20 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
25 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

- (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;
- (e) is the complement of the nucleotide sequence of (d);

- (f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;
- (g) is the complement of the nucleotide sequence of (f);
- (h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID
 NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID
 NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID
 NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
 5 NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID
 NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID
 NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID
 NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID
 NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID
 10 NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID
 NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID
 NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID
 NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID
 NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID
 15 NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID
 NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID
 NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID
 NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID
 NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID
 20 NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID
 NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID
 NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
 NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not
 all, of the domains selected from the group consisting of an N-terminal domain, a catalytic
 25 domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure
 region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or promoter effective to initiate transcription in a host cell.

4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of
5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
10 SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

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7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

5 ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
10 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
15 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
20 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
25 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090, N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, 15 AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
 ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
 ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
 5 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
 ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ
 ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
 ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
 ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
 10 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
 ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
 ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
 ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
 ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
 15 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
 ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
 ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
 ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
 ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
 20 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
 ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
 SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
 ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
 25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
 ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
 ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
 ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
 ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
 30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
 ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

5 ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
10 ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
15 ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from
the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a
spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set
20 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
25 NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID
NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID
30 NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID
NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,
5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242 with a test substance;

(b) measuring the activity of said polypeptide; and
(c) determining whether said substance modulates the activity of said
25 polypeptide.

30. A method for identifying a substance that modulates kinase activity in a
cell comprising:

(a) expressing a kinase polypeptide in a cell, wherein said polypeptide
is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID
30 NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
5 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID
10 NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID
15 NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
20 NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

- (b) adding a test substance to said cell; and
- (c) monitoring a change in cell phenotype or the interaction between
said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

- (a) contacting said sample with a nucleic acid probe which hybridizes
5 under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
10 SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
15 SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
20 SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
25 SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
30 SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

- 5 (b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

Table 1

[illegible]

Table 1 (cont'd)

Gene Name	SP	Prox. Seq. ID NA	Prox. Seq. ID AA	SEQ. ID # na	SEQ. ID # aa	Family	Group	Length NA	Length AA	ORF Start	ORF end	ORF Length	DNA Repeats	CHR localization
BCO3 h	M	146	184	84	184	Other	C26C2 ce	2164	536	113	1717	1606	246-287	NA
AA711829 m	M	146	184	85	185	Other	C26C2 ce	1568	378	1	1134	1134	NA	NA
AA096102 h CAAKCB	M	132	188	86	186	Other	CAMAKC	1787	588	1	1784	1784	65-84	12p23-q14
SRB9 17.2 h	M	159	194	87	197	Other	CTR1	3387	241	1850	3695	723	489-521	NA
HB5811 h	M	134	170	88	188	Other	DYRK	3693	1171	183	3695	3513	1325-1348	OS-PR7
AA02103 h DTRK3	M	133	169	89	189	Other	DYRK	2141	553	253	1911	1659	NA	NA
AA586241 m DTRK3 m	M	133	169	70	190	Other	DYRK	741	188	3	500	504	NA	NA
SR72 16.2 h R18023 h	M	109	112	71	191	Other	EFK	5163	1549	20	4950	4947	NA	NA
R43524 h RRI h R19009 h	M	111	114	72	182	Other	EFK	1863	630	1	1860	1860	NA	7p22-p22.3
1700057519457 h	M	135	171	73	193	Other	Endop	3055	253	219	377	759	2385-2385	NA
AA013524 m	M	135	171	74	194	Other	Endop	928	218	1	448	648	NA	NA
17000139801187 h IRAK4	M	137	173	75	195	Other	IRAK	1791	598	1	1788	1788	NA	NA
AA040598 m IRAK4 m	M	137	173	76	196	Other	IRAK	2243	392	1	1175	1175	NA	NA
AA088547 h	M	138	174	77	197	Other	IRE	2768	922	1	2768	2768	NA	NA
HGP 8644469	M	138	174	78	198	Other	IRE	1857	322	170	1144	966	NA	NA
AA489542 m	M	139	175	80	199	Other	KYX2 ad	1281	280	2	841	840	602-621	NA
5657 10.2 m TESK2 m	M	115	116	81	200	Other	LMK	140	41	2	124	123	NA	NA
AA322553 h	M	117	118	82	201	Other	LMK	2403	600	1	2400	2400	NA	NA
AA376137 h	M	209	210	83	202	Other	MRK	2508	835	1	2505	2505	2219-2238	NA
191685 h	M	143	178	84	203	Other	RIP	3384	634	181	2082	1902	NA	10q1
172810 m	M	144	180	85	204	Other	RIP	1073	289	3	889	887	NA	10q2
AA142336 h	M	211	212	86	205	Other	SC11 ac	2687	685	1	2684	2684	NA	NA
AA052750 h	M	225	226	87	206	Other	SC11 ac	1738	385	174	1588	1515	1784-1785	11p12-q13 Amplikon
AA218842 h	M	164	200	88	207	Other	SC11 ac	2688	808	105	2328	2424	NA	NA
AA096286 h	M	145	181	89	208	Other	SLOB7	1949	645	1	1948	1949	NA	NA
AA425725 h	M	146	182	90	209	Other	SOPK	1602	533	1	1598	1599	NA	NA
SGK022 h	M	148	185	91	210	Other	STR2A	1008	288	194	950	804	NA	NA
AA060026 m SGK022 m	M	148	185	92	211	Other	STR2A	1004	288	147	950	804	NA	NA
AA599689 h	M	150	186	93	212	Other	STR2A	1537	292	372	1244	1074	NA	1p11-q11
AA756539 h	M	151	187	94	213	Other	STR2A	1322	358	101	1174	1074	NA	NA
AA053975 h	M	153	189	95	214	Other	TSK	822	273	1	819	819	NA	NA
AA054446 h	M	223	224	96	215	Other	TSK	1068	218	365	1012	845	NA	NA
129974 h	M	88	102	97	216	Other	UNC	1638	333	2	1000	899	NA	NA
AA488104 m 129974 m	M	88	102	97	216	Other	UNC	1638	333	2	1000	899	NA	NA
AA215311 h	M	155	191	98	217	Other	UNC	1480	412	1	1258	1236	701-720	NA
AA016361 h	M	154	190	99	218	Other	UNC	2011	341	189	1221	1023	NA	NA
AA311714 h	M	156	192	101	220	Other	UNC	2759	481	113	1555	1443	NA	15q23
SGK384 h	M	156	192	101	220	Other	UNC	1870	565	135	1833	1685	NA	NA
AA210451 m SGK384 m	M	156	192	102	221	Other	Unique	117	39	1	117	117	NA	NA
SGK071.2 h	M	156	192	103	222	Other	Unique	2721	349	222	1288	1047	225-2286	NA
SGK071.2 h	M	156	192	104	223	Other	Unique	2115	704	1	2112	2112	37-76, 318-337	NA
AA118332 m SGK071 m	M	161	197	105	224	Other	Unique	1729	540	3	1822	1820	NA	NA
019533 h	M	162	198	106	225	Other	Unique	2481	540	1	1820	1820	240-259	NA
AA396501 m	M	163	199	107	226	Other	Unique	1888	385	3	1087	1085	NA	NA
AA071275 h VRK3	M	163	199	108	227	Other	VRK	1425	474	1	1422	1422	NA	18q13
571575 m VRK3 m	M	163	199	108	227	Other	VRK	1030	234	3	704	702	637-687	NA
AA452647 h MPKSK1	M	139	172	109	228	Other	YKL238 ac	918	305	1	915	915	NA	2cen-3q21
H05731 h	M	168	202	110	229	Other	YKL238 ac	2688	581	65	1837	1743	NA	1p32.3-31 Amplikon
AA08865 h	M	168	202	111	230	Other	NEK	2483	698	7	2100	2094	NA	NA
AA030348 h	M	130	124	113	232	Other	NEK	2511	638	1	2508	2508	NA	NA
RR6668 h UNK6	M	121	125	114	233	Other	STR11	3638	1011	1	3033	3033	NA	1p32.3-p11.1
PAK5 h 5485-23-11	M	219	220	115	234	Other	STR11	2180	719	1	2157	2157	NA	20p12
SGR1K106 h 2941-9-4 h	M	128,127	128,130	116	235	Other	STR2A02	2488	485	1	1485	1485	NA	13p12.3
AA098024 m	M	128,127	130	117	236	Other	STR2A02	1783	485	1	549	549	13p12.3	NA
SGK2394 h	M	118	118	118	237	Other	STR2A02	1812	387	88	1188	1107	NA	NA
H08950 h CORK	M	67	101	120	238	Other	STR2A02	1356	432	1	1356	1356	NA	1p21.1-q21.3
NA 007170 h TESK2	M	1	1	121	239	Other	UNK	3016	555	386	2680	1685	NA	NA

Table 2

SP	Patent Seq	Seq ID# aa	Family	Group	nrseq	Length aa	ID match	% Identity	% Similar	Match ACCs	Description	Kinase Domain(s) start	Kinase Domain(s) end	Profile start	Profile end
H 1	122	122	AGC	GRK	2.7E-314	688	687	100	100	CAB45657.1	BAR2 [Homo sapiens]	191	453	1	281
M 2	123	123	AGC	GRK	1.30E-180	378	371	98	99	NP 037028.1	Adrenergic receptor kinase, beta 2 (G-protein-linked receptor) [Homo sapiens]	3	143	121	281
M 3	124	124	AGC	GRK	5.80E-106	419	262	71	86	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	28	288	1	281
H 4	125	125	AGC	GRK	1.40E-137	414	414	100	100	CAB76471.1	Serine/threonine protein kinase [Homo sapiens]	23	283	1	281
H 5	128	128	AGC	GRK	0	728	728	100	100	NP 037386.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	281
M 6	127	127	AGC	NDR	1.20E-09	329	73	48	66	BAA76817.1	KIAA0973 protein [Homo sapiens]	35	310	1	281
M 7	128	128	AGC	NDR	1.30E-19	88	42	48	71	AAF55594.1	CG7179 gene product [Drosophila melanogaster]	24	44	242	281
M 8	129	129	AGC	NDR	6.10E-181	454	453	100	100	BAA76809.1	KIAA0965 protein [Homo sapiens]	90	383	1	281
H 9	130	130	AGC	PKC	8.80E-160	978	615	67	80	NP 002733.1	Protein kinase C, nu [Homo sapiens]	851	907	1	281
H 10	131	131	AGC	PKC	1.10E-10	105	42	42	57	P05127	Protein kinase C, BETA-II TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256	281
H 11	132	132	AGC	PKC	0	890	889	100	100	NP 035804.1	Protein kinase C, nu [Homo sapiens]	578	832	1	281
H 12	133	133	AGC	PKC	9.4E-319	889	889	100	100	NP 037487.1	PKNbeta [Homo sapiens]	559	818	1	281
M 13	134	134	AGC	PKC	1.20E-106	205	204	100	100	JC7083	Protein kinase N beta [Homo sapiens]	1	134	128	281
H 14	135	135	AGC	SGK	3.60E-12	354	94	38	55	AAC82495.1	Protein kinase N beta [Homo sapiens]	81	333	1	281
H 15	136	136	AGC	SGK	2.90E-257	469	469	100	100	NP 036556.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	225	459	1	281
H 16	137	137	AGC	SGK	7.00E-178	745	745	100	100	NP 055311.1	Ribosomal protein S6 kinase, 52kD, polypeptide 1 [Homo sapiens]	330 & 683	1	281	281
H 17	138	138	AGC	SGK	8.60E-222	549	549	100	100	AA030182.1	Ribosomal protein S6 kinase, 60kD, polypeptide 8 [Homo sapiens]	153	539	1	281
H 18	139	139	AGC	SGK	9.20E-103	431	430	100	100	AA041091.1	Unknown [Homo sapiens]	98	355	1	281
M 19	140	140	AGC	SGK	2.80E-157	430	429	99	99	NP 035481.1	Serum/glucocorticoid regulated kinase [Mus musculus]	98	354	1	281
M 20	141	141	AGC	SGK	2.00E-76	244	244	100	100	AAF12757.2	Protein kinase [Homo sapiens]	1	169	24	281
H 21	142	142	AGC	SGK	4.10E-211	446	375	88	88	AAF27051.1	SGK-like protein SGK [Homo sapiens]	182	369	1	281
H 22	143	143	AGC	SGK	5.60E-216	349	349	100	100	NP 009215.1	Protein tyrosine kinase 9-like (A6-related protein) [Homo sapiens]	10	17	253	281
H 23	144	144	CAMK	AMPK	1.40E-19	440	68	39	61	CAA04119.1	Phosphoinositide 3-kinase [Homo sapiens]	40	333	1	281
H 24	145	145	CAMK	AMPK	1.50E-165	889	468	65	77	O15075	DCAMK1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1) [Homo sapiens]	368	625	1	281
M 25	146	146	CAMK	AMPK	1.80E-82	297	199	67	83	AAF26675.1	CPG16 [Mus musculus]	59	287	1	281
M 26	147	147	CAMK	AMPK	2.60E-48	708	181	44	60	AAF26675.1	CPG16 [Mus musculus]	514	771	1	281
M 28	148	148	CAMK	AMPK	2.60E-31	808	147	55	73	NP 004217.1	Death-associated protein kinase-related 2	33	293	1	281
M 29	149	149	CAMK	AMPK	3.10E-121	372	372	100	100	NP 004217.1	Death-associated protein kinase-related 2	32	293	1	281
M 30	150	150	CAMK	AMPK	7.90E-83	372	340	91	95	NP 004217.1	Death-associated protein kinase-related 2	32	293	1	281
H 31	151	151	CAMK	AMPK	1.20E-113	414	414	100	100	NP 004751.1	Death-associated protein kinase-related 1	61	321	1	281
H 32	152	152	CAMK	AMPK	5.90E-185	1311	1053	80	80	BAA76843.1	KIAA0989 protein [Homo sapiens]	8	259	1	281
H 33	153	153	CAMK	AMPK	1.20E-45	438	153	51	70	T22427	Hypothetical protein F49C5.4 - [Caenorhabditis elegans]	74	325	1	281
H 34	154	154	CAMK	AMPK	1.40E-32	439	122	48	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	281
H 35	155	155	CAMK	AMPK	1.30E-184	729	728	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	59	340	1	281
M 36	156	156	CAMK	AMPK	3.50E-128	462	462	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	989	1258	1	281
M 37	157	157	CAMK	AMPK	0	1330	1235	100	100	BA009484.1	KIAA0135 gene, related to p11-1 oncogene, [Homo sapiens]	1	158	23	281
M 38	158	158	CAMK	AMPK	5.10E-59	230	183	78	85	BA009484.1	KIAA0135 gene, related to p11-1 oncogene, [Homo sapiens]	20	271	1	281
H 39	159	159	CAMK	AMPK	3.00E-111	926	636	100	100	BAA34501.1	KIAA0761 protein [Homo sapiens]	53	304	1	281
H 40	160	160	CAMK	AMPK	7.30E-80	628	367	57	69	NP 055655.1	KIAA0537 gene product [Homo sapiens]	53	304	1	281
H 41	161	161	CAMK	AMPK	1.40E-244	714	714	100	100	NP 055655.1	KIAA0537 gene product [Homo sapiens]	61	320	1	281
H 42	162	162	CAMK	AMPK	8.20E-76	874	211	63	80	AA073168.1	Homodimeric upregulated new tumor-associated kinase [Homo sapiens]	570	825	1	281
H 43	163	163	CAMK	AMPK	0	2288	2227	100	100	AA073168.1	Skeletal muscle myosin light chain kinase [Gallus gallus]	920 & 1086	873 & 1356	1	281
M 44	164	164	CAMK	AMPK	7.80E-37	127	67	99	99	BAA92535.1	KIAA1267 protein [Homo sapiens]	3	78	186	281
H 45	165	165	CAMK	AMPK	0	1287	1284	100	100	NP 008895.1	STK with Dbl- and pleckstrin homology domains [Homo sapiens]	985	1239	1	281
H 46	166	166	CKI	CKI	5.00E-20	514	114	41	63	P25323	MLCK [Drosophila melanogaster]	116	381	1	281
H 47	167	167	CKI	CKI	3.30E-89	508	181	53	65	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	34	313	1	281
H 48	168	168	CMGC	CMGC	8.60E-98	478	188	57	68	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	21	471	1	281
H 49	169	169	CMGC	CMGC	9.60E-39	266	138	62	79	NP 036527.1	PF-TAIRE protein kinase 1 [Homo sapiens]	1	218	23	281
H 50	170	170	CMGC	CMGC	7.10E-46	247	146	59	75	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	181	23	281

Table 2 (cont'd)

M	50	170	CMGC	CDK	2.80E-44	296	193	65	78	NP_004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	240	24	261
H	51	171	CMGC	CDK	1.10E-264	1490	1490	100	100	AAF38401.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H	52	172	CMGC	CDK	9.20E-101	534	377	82	82	AAF38509.1	NKIATRE [Homo sapiens]	4	385	1	261
M	53	173	CMGC	CDK	1.40E-128	337	225	92	86	AAF34871.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M	54	174	CMGC	CDK	3.00E-98	211	159	79	84	NP_038251.1	Cell cycle related kinase [Homo sapiens]	1	153	134	261
H	55	175	CMGC	CLK	1.50E-242	489	436	91	93	NP_031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	177	483	1	261
H	56	176	CMGC	RCK	9.10E-88	544	343	57	64	NP_031740.1	Extracellular signal-regulated kinase 7, ERK7 [Rattus norvegicus]	13	305	1	261
H	57	177	CMGC	RCK	2.30E-189	419	419	100	100	NP_055041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
H	58	178	CMGC	RCK	1.50E-180	632	632	100	100	AAF37278.1	Intestinal cell kinase [Homo sapiens]	4	284	1	261
M	59	179	CMGC	RCK	1.60E-78	413	188	60	77	P20689	MLCK [Rattus norvegicus]	109	384	1	261
H	60	180	Microbial PK	YGR262.ac	2.60E-45	253	102	46	67	AAF50789.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
H	61	181	Other	C26C2.cb	2.30E-156	509	258	100	100	CAB70864.1	Hypothetical protein [Homo sapiens]	2	287	1	261
M	62	182	Other	C26C2.cb	1.80E-152	281	243	94	98	CAB70864.1	Hypothetical protein [Homo sapiens]	59	86	235	261
H	63	183	Other	C26C2.cb	6.70E-300	1952	1193	99	99	NP_055638.1	KIAA0344 gene product [Homo sapiens]	221	479	1	261
H	64	184	Other	C26C2.cb	1.10E-254	535	535	100	100	NP_037524.1	Nuclear receptor binding protein [Homo sapiens]	73	327	1	261
M	65	185	Other	C26C2.cb	2.50E-208	378	372	98	100	NP_037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
H	66	186	Other	CAMKK	3.80E-148	588	588	100	100	AAO31507.1	Ca2+/calmodulin-dependent protein kinase beta [Homo sapiens]	165	448	1	261
H	67	187	Other	CTRI	9.90E-24	287	87	33	52	JQ1743	Hypothetical 33.6K protein - rabbit fibroma virus	24	285	1	261
H	68	188	Other	DYRK	0	1171	1137	87	89	AAO52566.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H	69	189	Other	DYRK	2.10E-280	553	553	100	100	NP_003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	174	487	1	261
M	70	190	Other	DYRK	2.30E-95	168	149	90	96	NP_003573.1	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	76	103	235	261
H	71	191	Other	EIFK	0	1649	1493	90	88	NP_038747.1	GCN2 eIF2alpha kinase [Mus musculus]	280 & 590	539 & 1001	1	261
H	73	192	Other	EIFK	1.50E-220	630	630	100	100	NP_055228.1	Heme-regulated initiation factor 2-alpha kinase [Homo sapiens]	187	583	1	261
H	74	193	Other	Endop	2.50E-45	253	102	46	67	AAF50789.1	CG10673 gene product [Drosophila melanogaster]	101	187	65	147
M	75	194	Other	Endop	3.70E-45	216	100	45	64	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	165	443	1	261
H	76	195	Other	IRAK	0	586	586	100	100	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	1	239	19	261
M	77	196	Other	IRAK	1.20E-170	392	263	75	85	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	516	777	1	261
H	78	197	Other	IRE	1.5e-323	922	745	82	89	NP_038146.1	Irf1, Inositol-requiring 1 gene [Mus musculus]	32	318	1	261
H	79	198	Other	KYK2.dd	8.70E-40	225	102	45	62	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	12	268	1	261
M	80	199	Other	KYK2.dd	5.90E-32	280	109	32	50	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	12	268	1	261
M	81	200	Other	LMNK	2.60E-17	41	37	92	95	NP_009101.1	Leslie-specific kinase 2 [Homo sapiens]	12	39	101	128
H	82	201	Other	MLK	2.50E-282	800	799	100	100	AAF63490.1	Mixed lineage kinase [Homo sapiens]	18	259	1	261
H	83	202	Other	MLK	8.60E-251	835	835	100	100	AAO29632.1	Putative protein-tyrosine kinase [Homo sapiens]	463	723	1	261
H	84	203	Other	RIP	2.20E-158	634	385	100	100	BAA32317.1	KIAA0472 protein [Homo sapiens]	357	620	1	261
M	85	204	Other	RIP	5.30E-158	289	288	100	100	AAF03133.1	Receptor interacting protein 3 [Mus musculus]	7	27	181	202
H	86	205	Other	SCY1.sc	0	688	688	100	100	CAF55300.1	Hypothetical protein [Homo sapiens]	57	83	50	76
H	87	206	Other	SCY1.sc	1.70E-209	505	354	98	98	BAA92598.1	KIAA1360 protein [Homo sapiens]	32	327	1	261
H	88	207	Other	SCY1.sc	2.20E-157	808	396	45	61	AAF58933.1	CG1873 gene product [Drosophila melanogaster]	65	131	47	116
H	89	208	Other	SLOB7	7.40E-198	649	649	100	100	BAA91097.1	Unnamed protein product [Homo sapiens]	230	305	81	143
H	90	209	Other	SRPK	5.80E-252	533	533	100	100	NP_055185.1	Serine/threonine kinase 23 [Homo sapiens]	79	531	1	261
H	91	210	Other	STK22A	3.80E-53	268	122	48	70	NP_033461.1	Serine/threonine kinase 22A (germogenesis associated) [Mus musculus]	10	265	1	261
M	92	211	Other	STK22A	2.70E-52	268	127	48	68	NP_033461.1	Serine/threonine kinase 22B (germogenesis associated)	10	265	1	261
H	93	212	Other	STK22A	4.60E-16	262	112	45	64	NP_033461.1	Serine/threonine kinase 22A (germogenesis associated)	25	280	1	261
H	94	213	Other	STK22A	5.10E-123	358	322	90	98	NP_033462.1	Serine/threonine kinase 22B (germogenesis associated) [Mus musculus]	12	272	1	261
H	95	214	Other	TSK	2.10E-33	273	122	46	62	NP_033461.1	Serine/threonine kinase 22A (germogenesis associated)	12	267	1	261
H	96	215	Other	TSK	2.50E-32	216	83	41	58	NP_033462.1	Serine/threonine kinase 22B (germogenesis associated)	1	213	7	261
H	97	216	Other	UNC	0.000062	333	57	36	56	AAO32787.1	Putative protein kinase [Arabidopsis thaliana]	1	329	1	261
M	98	217	Other	UNC	0.002492	412	53	37	52	BAA77341.1	UNC-51-like kinase [ULK] 2 [Mus musculus]	80	408	1	261
H	99	218	Other	UNC	0.001096	341	50	36	56	BAA77341.1	UNC-51-like kinase [ULK] 2 [Mus musculus]	8	340	1	261
H	100	219	Other	UNC	1.90E-68	480	247	100	100	T17265	Hypothetical protein DKFZp434C131.1 - human (fragment)	57	313	1	261
H	101	220	Other	UNC	1.60E-208	565	468	96	96	BAA91270.1	Unamed protein product [Homo sapiens]	4	265	1	261
H	102	221	Other	Unique	6.70E-10	39	27	69	90	AAO00575.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

Table 2 (cont'd)

M 103	222	Other	Unique	0.000022	349	38	30	50	CAA18116.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana]	80	159	1	88
H 104	223	Other	Unique	0.000126	704	54	30	45	BAA86578.1	KIAA1284 protein [Homo sapiens]	1	246	25	281
M 105	224	Other	Unique	0.007385	540	25	42	61	AAF47916.1	The gene product [Drosophila melanogaster]	9	104	168	281
H 106	225	Other	Unique	0.31334	540	52	30	42	P10162	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo sapiens]	1	272	18	73
M 107	226	Other	Unique	0.022948	365	25	34	57	NP_006276.1	testis-specific kinase 1 [Homo sapiens]	68	66	42	71
H 108	227	Other	VRK	3.10E-263	474	474	100	100	BAA80769.1	Vaccinia related kinase 3 [Homo sapiens]	247	318	63	136
M 109	228	Other	VRK	1.20E-111	234	191	82	90	BAA80769.1	(AB031052) vaccinia related kinase 3 [Homo sapiens]	7	78	63	136
H 110	229	Other	YPL238 gc	7.40E-144	305	304	100	100	AAC28337.1	MPKSK [Homo sapiens]	20	280	1	281
H 111	230	Other	YQ06 ce	5.10E-49	581	135	43	63	AAF48188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H 112	231	STE	NEK	3.30E-30	698	122	48	67	P51854	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	251	1	281
H 113	232	STE	NEK	2.70E-119	838	357	88	86	AAD31939.1	(AC007065) unknown [Homo sapiens]	52	308	1	281
H 114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004663.1	mitogen-activated protein kinase kinase kinase 6 [Homo sapiens]	376	628	6	281
H 115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA94184.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	281
H 116	235	TK	RTK-20	4.80E-24	485	77	38	56	AAA88465.1	(U40827) protein tyrosine kinase [Mus musculus]	187	453	1	281
M 117	236	TK	RTK-20	5.30E-18	183	53	39	57	NP_032036.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	281
H 118	237	AGC	SGK	8.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	282	1	281
H 120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_039251.1	Cell cycle related kinase [Homo sapiens]	4	287	1	281
H 121	239	Other	LIMK	6.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	283	5	281

164
Table 3

Tissue	Tumor-ayn	Normal-ayn	Tumor - to	Tumor path	Normal	Endes	p53	MDM2	MDM4	MDM5	MDM6	MDM7	MDM8	MDM9	MDM10	MDM11	MDM12	MDM13	MDM14	MDM15	MDM16	MDM17	MDM18	MDM19	MDM20	MDM21	MDM22	MDM23	MDM24	MDM25	MDM26	MDM27	MDM28	MDM29	MDM30	MDM31	MDM32	MDM33	MDM34	MDM35	MDM36	MDM37	MDM38	MDM39	MDM40	MDM41	MDM42	MDM43	MDM44	MDM45	MDM46	MDM47	MDM48	MDM49	MDM50	MDM51	MDM52	MDM53	MDM54	MDM55	MDM56	MDM57	MDM58	MDM59	MDM60	MDM61	MDM62	MDM63	MDM64	MDM65	MDM66	MDM67	MDM68	MDM69	MDM70	MDM71	MDM72	MDM73	MDM74	MDM75	MDM76	MDM77	MDM78	MDM79	MDM80	MDM81	MDM82	MDM83	MDM84	MDM85	MDM86	MDM87	MDM88	MDM89	MDM90	MDM91	MDM92	MDM93	MDM94	MDM95	MDM96	MDM97	MDM98	MDM99	MDM100	MDM101	MDM102	MDM103	MDM104	MDM105	MDM106	MDM107	MDM108	MDM109	MDM110	MDM111	MDM112	MDM113	MDM114	MDM115	MDM116	MDM117	MDM118	MDM119	MDM120	MDM121	MDM122	MDM123	MDM124	MDM125	MDM126	MDM127	MDM128	MDM129	MDM130	MDM131	MDM132	MDM133	MDM134	MDM135	MDM136	MDM137	MDM138	MDM139	MDM140	MDM141	MDM142	MDM143	MDM144	MDM145	MDM146	MDM147	MDM148	MDM149	MDM150	MDM151	MDM152	MDM153	MDM154	MDM155	MDM156	MDM157	MDM158	MDM159	MDM160	MDM161	MDM162	MDM163	MDM164	MDM165	MDM166	MDM167	MDM168	MDM169	MDM170	MDM171	MDM172	MDM173	MDM174	MDM175	MDM176	MDM177	MDM178	MDM179	MDM180	MDM181	MDM182	MDM183	MDM184	MDM185	MDM186	MDM187	MDM188	MDM189	MDM190	MDM191	MDM192	MDM193	MDM194	MDM195	MDM196	MDM197	MDM198	MDM199	MDM200	MDM201	MDM202	MDM203	MDM204	MDM205	MDM206	MDM207	MDM208	MDM209	MDM210	MDM211	MDM212	MDM213	MDM214	MDM215	MDM216	MDM217	MDM218	MDM219	MDM220	MDM221	MDM222	MDM223	MDM224	MDM225	MDM226	MDM227	MDM228	MDM229	MDM230	MDM231	MDM232	MDM233	MDM234	MDM235	MDM236	MDM237	MDM238	MDM239	MDM240	MDM241	MDM242	MDM243	MDM244	MDM245	MDM246	MDM247	MDM248	MDM249	MDM250	MDM251	MDM252	MDM253	MDM254	MDM255	MDM256	MDM257	MDM258	MDM259	MDM260	MDM261	MDM262	MDM263	MDM264	MDM265	MDM266	MDM267	MDM268	MDM269	MDM270	MDM271	MDM272	MDM273	MDM274	MDM275	MDM276	MDM277	MDM278	MDM279	MDM280	MDM281	MDM282	MDM283	MDM284	MDM285	MDM286	MDM287	MDM288	MDM289	MDM290	MDM291	MDM292	MDM293	MDM294	MDM295	MDM296	MDM297	MDM298	MDM299	MDM300	MDM301	MDM302	MDM303	MDM304	MDM305	MDM306	MDM307	MDM308	MDM309	MDM310	MDM311	MDM312	MDM313	MDM314	MDM315	MDM316	MDM317	MDM318	MDM319	MDM320	MDM321	MDM322	MDM323	MDM324	MDM325	MDM326	MDM327	MDM328	MDM329	MDM330	MDM331	MDM332	MDM333	MDM334	MDM335	MDM336	MDM337	MDM338	MDM339	MDM340	MDM341	MDM342	MDM343	MDM344	MDM345	MDM346	MDM347	MDM348	MDM349	MDM350	MDM351	MDM352	MDM353	MDM354	MDM355	MDM356	MDM357	MDM358	MDM359	MDM360	MDM361	MDM362	MDM363	MDM364	MDM365	MDM366	MDM367	MDM368	MDM369	MDM370	MDM371	MDM372	MDM373	MDM374	MDM375	MDM376	MDM377	MDM378	MDM379	MDM380	MDM381	MDM382	MDM383	MDM384	MDM385	MDM386	MDM387	MDM388	MDM389	MDM390	MDM391	MDM392	MDM393	MDM394	MDM395	MDM396	MDM397	MDM398	MDM399	MDM400	MDM401	MDM402	MDM403	MDM404	MDM405	MDM406	MDM407	MDM408	MDM409	MDM410	MDM411	MDM412	MDM413	MDM414	MDM415	MDM416	MDM417	MDM418	MDM419	MDM420	MDM421	MDM422	MDM423	MDM424	MDM425	MDM426	MDM427	MDM428	MDM429	MDM430	MDM431	MDM432	MDM433	MDM434	MDM435	MDM436	MDM437	MDM438	MDM439	MDM440	MDM441	MDM442	MDM443	MDM444	MDM445	MDM446	MDM447	MDM448	MDM449	MDM450	MDM451	MDM452	MDM453	MDM454	MDM455	MDM456	MDM457	MDM458	MDM459	MDM460	MDM461	MDM462	MDM463	MDM464	MDM465	MDM466	MDM467	MDM468	MDM469	MDM470	MDM471	MDM472	MDM473	MDM474	MDM475	MDM476	MDM477	MDM478	MDM479	MDM480	MDM481	MDM482	MDM483	MDM484	MDM485	MDM486	MDM487	MDM488	MDM489	MDM490	MDM491	MDM492	MDM493	MDM494	MDM495	MDM496	MDM497	MDM498	MDM499	MDM500	MDM501	MDM502	MDM503	MDM504	MDM505	MDM506	MDM507	MDM508	MDM509	MDM510	MDM511	MDM512	MDM513	MDM514	MDM515	MDM516	MDM517	MDM518	MDM519	MDM520	MDM521	MDM522	MDM523	MDM524	MDM525	MDM526	MDM527	MDM528	MDM529	MDM530	MDM531	MDM532	MDM533	MDM534	MDM535	MDM536	MDM537	MDM538	MDM539	MDM540	MDM541	MDM542	MDM543	MDM544	MDM545	MDM546	MDM547	MDM548	MDM549	MDM550	MDM551	MDM552	MDM553	MDM554	MDM555	MDM556	MDM557	MDM558	MDM559	MDM560	MDM561	MDM562	MDM563	MDM564	MDM565	MDM566	MDM567	MDM568	MDM569	MDM570	MDM571	MDM572	MDM573	MDM574	MDM575	MDM576	MDM577	MDM578	MDM579	MDM580	MDM581	MDM582	MDM583	MDM584	MDM585	MDM586	MDM587	MDM588	MDM589	MDM590	MDM591	MDM592	MDM593	MDM594	MDM595	MDM596	MDM597	MDM598	MDM599	MDM600	MDM601	MDM602	MDM603	MDM604	MDM605	MDM606	MDM607	MDM608	MDM609	MDM610	MDM611	MDM612	MDM613	MDM614	MDM615	MDM616	MDM617	MDM618	MDM619	MDM620	MDM621	MDM622	MDM623	MDM624	MDM625	MDM626	MDM627	MDM628	MDM629	MDM630	MDM631	MDM632	MDM633	MDM634	MDM635	MDM636	MDM637	MDM638	MDM639	MDM640	MDM641	MDM642	MDM643	MDM644	MDM645	MDM646	MDM647	MDM648	MDM649	MDM650	MDM651	MDM652	MDM653	MDM654	MDM655	MDM656	MDM657	MDM658	MDM659	MDM660	MDM661	MDM662	MDM663	MDM664	MDM665	MDM666	MDM667	MDM668	MDM669	MDM670	MDM671	MDM672	MDM673	MDM674	MDM675	MDM676	MDM677	MDM678	MDM679	MDM680	MDM681	MDM682	MDM683	MDM684	MDM685	MDM686	MDM687	MDM688	MDM689	MDM690	MDM691	MDM692	MDM693	MDM694	MDM695	MDM696	MDM697	MDM698	MDM699	MDM700	MDM701	MDM702	MDM703	MDM704	MDM705	MDM706	MDM707	MDM708	MDM709	MDM710	MDM711	MDM712	MDM713	MDM714	MDM715	MDM716	MDM717	MDM718	MDM719	MDM720	MDM721	MDM722	MDM723	MDM724	MDM725	MDM726	MDM727	MDM728	MDM729	MDM730	MDM731	MDM732	MDM733	MDM734	MDM735	MDM736	MDM737	MDM738	MDM739	MDM740	MDM741	MDM742	MDM743	MDM744	MDM745	MDM746	MDM747	MDM748	MDM749	MDM750	MDM751	MDM752	MDM753	MDM754	MDM755	MDM756	MDM757	MDM758	MDM759	MDM760	MDM761	MDM762	MDM763	MDM764	MDM765	MDM766	MDM767	MDM768	MDM769	MDM770	MDM771	MDM772	MDM773	MDM774	MDM775	MDM776	MDM777	MDM778	MDM779	MDM780	MDM781	MDM782	MDM783	MDM784	MDM785	MDM786	MDM787	MDM788	MDM789	MDM790	MDM791	MDM792	MDM793	MDM794	MDM795	MDM796	MDM797	MDM798	MDM799	MDM800	MDM801	MDM802	MDM803	MDM804	MDM805	MDM806	MDM807	MDM808	MDM809	MDM810	MDM811	MDM812	MDM813	MDM814	MDM815	MDM816	MDM817	MDM818	MDM819	MDM820	MDM821	MDM822	MDM823	MDM824	MDM825	MDM826	MDM827	MDM828	MDM829	MDM830	MDM831	MDM832	MDM833	MDM834	MDM835	MDM836	MDM837	MDM838	MDM839	MDM840	MDM841	MDM842	MDM843	MDM844	MDM845	MDM846	MDM847	MDM848	MDM849	MDM850	MDM851	MDM852	MDM853	MDM854	MDM855	MDM856	MDM857	MDM858	MDM859	MDM860	MDM861	MDM862	MDM863	MDM864	MDM865	MDM866	MDM867	MDM868	MDM869	MDM870	MDM871	MDM872	MDM873	MDM874	MDM875	MDM876	MDM877	MDM878	MDM879	MDM880	MDM881	MDM882	MDM883	MDM884	MDM885	MDM886	MDM887	MDM888	MDM889	MDM890	MDM891	MDM892	MDM893	MDM894	MDM895	MDM896	MDM897	MDM898	MDM899	MDM900	MDM901	MDM902	MDM903	MDM904	MDM905	MDM906	MDM907	MDM908	MDM909	MDM910	MDM911	MDM912	MDM913	MDM914	MDM915	MDM916	MDM917	MDM918	MDM919	MDM920	MDM921	MDM922	MDM923	MDM924	MDM925	MDM926	MDM927	MDM928	MDM929	MDM930	MDM931	MDM932	MDM933	MDM934	MDM935	MDM936	MDM937	MDM938	MDM939	MDM940	MDM941	MDM942	MDM943	MDM944	MDM945	MDM946	MDM947	MDM948	MDM949	MDM950	MDM951	MDM952	MDM953	MDM954	MDM955	MDM956	MDM957	MDM958	MDM959	MDM960	MDM961	MDM962	MDM963	MDM964	MDM965	MDM966	MDM967	MDM968	MDM969	MDM970	MDM971	MDM972	MDM973	MDM974	MDM975	MDM976	MDM977	MDM978	MDM979	MDM980	MDM981	MDM982	MDM983	MDM984	MDM985	MDM986	MDM987	MDM988	MDM989	MDM990	MDM991	MDM992	MDM993	MDM994	MDM995	MDM996	MDM997	MDM998	MDM999	MDM1000	MDM1001	MDM1002	MDM1003	MDM1004	MDM1005	MDM1006	MDM1007	MDM1008	MDM1009	MDM1010	MDM1011	MDM1012	MDM1013	MDM1014	MDM1015	MDM1016	MDM1017	MDM1018	MDM1019	MDM1020	MDM1021	MDM1022	MDM1023	MDM1024	MDM1025	MDM1026	MDM1027	MDM1028	MDM1029	MDM1030	MDM1031	MDM1032	MDM1033	MDM1034	MDM1035	MDM1036	MDM1037	MDM1038	MDM1039	MDM1040	MDM1041	MDM1042	MDM1043	MDM1044	MDM1045	MDM1046	MDM1047	MDM1048	MDM1049	MDM1050	MDM1051	MDM1052	MDM1053	MDM1054	MDM1055	MDM1056	MDM1057	MDM1058	MDM1059	MDM1060	MDM1061	MDM1062	MDM1063	MDM1064	MDM1065	MDM1066	MDM1067	MDM1068	MDM1069	MDM1070	MDM1071	MDM1072	MDM1073	MDM1074	MDM1075	MDM1076	MDM1077	MDM1078	MDM1079	MDM1080	MDM1081	MDM1082	MDM1083	MDM1084	MDM1085	MDM1086	MDM1087	MDM1088	MDM1089	MDM1090	MDM1091	MDM1092	MDM1093	MDM1094	MDM1095	MDM1096	MDM1097	MDM1098	MDM1099	MDM1100	MDM1101	MDM1102	MDM1103	MDM1104	MDM1105	MDM1106	MDM1107	MDM1108	MDM1109	MDM1110	MDM1111	MDM1112	MDM1113	MDM1114	MDM1115	MDM1116	MDM1117	MDM1118	MDM1119	MDM1120	MDM1121	MDM1122	MDM1123	MDM1124	MDM1125	MDM1126	MDM1127	MDM1128	MDM1129	MDM1130	MDM1131	MDM1132	MDM1133	MDM1134	MDM1135	MDM1136	MDM1137	MDM1138	MDM1139	MDM1140	MDM1141	MDM1142	MDM1143	MDM1144	MDM1145	MDM1146	MDM1147	MDM1148	MDM1149	MDM1150	MDM1151	MDM1152	MDM1153	MDM1154	MDM1155	MDM1156	MDM1157	MDM1158	MDM1159	MDM1160	MDM1161	MDM1162	MDM1163	MDM1164	MDM1165	MDM1166	MDM1167	MDM1168	MDM1169	MDM1170	MDM1171	MDM1172	MDM1173	MDM1174	MDM1175	MDM1176	MDM1177	MDM1178	MDM1179	MDM1180	MDM1181	MDM1182	MDM1183	MDM1184	MDM1185	MDM1186	MDM1187	MDM1188	MDM1189	MDM1190	MDM1191	MDM1192	MDM1193	MDM1194	MDM1195	MDM1196	MDM1197	MDM1198	MDM1199	MDM1200	MDM1201	MDM1202	MDM1203	MDM1204	MDM1205	MDM1206	MDM1207	MDM1208	MDM1209
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165
Table 3 (cont'd)

[illegible]

166
Table 3 (cont'd)

167
Table 3 (cont'd)[illegible]

169
Table 3 (cont'd)

Accession	Transcript	Normalcy	Yeast - 5s	Yeast poly	Normal	Ends	EST	SEQ 34	TRIG 43	ANEG 47	ANEG 48	ANEG 49	ANEG 50	ANEG 51	ANEG 52	ANEG 54	ANEG 55	ANEG 56	ANEG 57	ANEG 58	ANEG 59	ANEG 60	ANEG 61	ANEG 62	ANEG 63	ANEG 64	ANEG 65	ANEG 66	ANEG 67	ANEG 68	ANEG 69	ANEG 70	ANEG 71	ANEG 72	ANEG 73	ANEG 74	ANEG 75	ANEG 76	ANEG 77	ANEG 78	ANEG 79	ANEG 80	ANEG 81	ANEG 82	ANEG 83	ANEG 84	ANEG 85	ANEG 86	ANEG 87	ANEG 88	ANEG 89	ANEG 90	ANEG 91	ANEG 92	ANEG 93	ANEG 94	ANEG 95	ANEG 96	ANEG 97	ANEG 98	ANEG 99	ANEG 100	ANEG 101	ANEG 102	ANEG 103	ANEG 104	ANEG 105	ANEG 106	ANEG 107	ANEG 108	ANEG 109	ANEG 110	ANEG 111	ANEG 112	ANEG 113	ANEG 114	ANEG 115	ANEG 116	ANEG 117	ANEG 118	ANEG 119	ANEG 120	ANEG 121	ANEG 122	ANEG 123	ANEG 124	ANEG 125	ANEG 126	ANEG 127	ANEG 128	ANEG 129	ANEG 130	ANEG 131	ANEG 132	ANEG 133	ANEG 134	ANEG 135	ANEG 136	ANEG 137	ANEG 138	ANEG 139	ANEG 140	ANEG 141	ANEG 142	ANEG 143	ANEG 144	ANEG 145	ANEG 146	ANEG 147	ANEG 148	ANEG 149	ANEG 150	ANEG 151	ANEG 152	ANEG 153	ANEG 154	ANEG 155	ANEG 156	ANEG 157	ANEG 158	ANEG 159	ANEG 160	ANEG 161	ANEG 162	ANEG 163	ANEG 164	ANEG 165	ANEG 166	ANEG 167	ANEG 168	ANEG 169	ANEG 170	ANEG 171	ANEG 172	ANEG 173	ANEG 174	ANEG 175	ANEG 176	ANEG 177	ANEG 178	ANEG 179	ANEG 180	ANEG 181	ANEG 182	ANEG 183	ANEG 184	ANEG 185	ANEG 186	ANEG 187	ANEG 188	ANEG 189	ANEG 190	ANEG 191	ANEG 192	ANEG 193	ANEG 194	ANEG 195	ANEG 196	ANEG 197	ANEG 198	ANEG 199	ANEG 200	ANEG 201	ANEG 202	ANEG 203	ANEG 204	ANEG 205	ANEG 206	ANEG 207	ANEG 208	ANEG 209	ANEG 210	ANEG 211	ANEG 212	ANEG 213	ANEG 214	ANEG 215	ANEG 216	ANEG 217	ANEG 218	ANEG 219	ANEG 220	ANEG 221	ANEG 222	ANEG 223	ANEG 224	ANEG 225	ANEG 226	ANEG 227	ANEG 228	ANEG 229	ANEG 230	ANEG 231	ANEG 232	ANEG 233	ANEG 234	ANEG 235	ANEG 236	ANEG 237	ANEG 238	ANEG 239	ANEG 240	ANEG 241	ANEG 242	ANEG 243	ANEG 244	ANEG 245	ANEG 246	ANEG 247	ANEG 248	ANEG 249	ANEG 250	ANEG 251	ANEG 252	ANEG 253	ANEG 254	ANEG 255	ANEG 256	ANEG 257	ANEG 258	ANEG 259	ANEG 260	ANEG 261	ANEG 262	ANEG 263	ANEG 264	ANEG 265	ANEG 266	ANEG 267	ANEG 268	ANEG 269	ANEG 270	ANEG 271	ANEG 272	ANEG 273	ANEG 274	ANEG 275	ANEG 276	ANEG 277	ANEG 278	ANEG 279	ANEG 280	ANEG 281	ANEG 282	ANEG 283	ANEG 284	ANEG 285	ANEG 286	ANEG 287	ANEG 288	ANEG 289	ANEG 290	ANEG 291	ANEG 292	ANEG 293	ANEG 294	ANEG 295	ANEG 296	ANEG 297	ANEG 298	ANEG 299	ANEG 300	ANEG 301	ANEG 302	ANEG 303	ANEG 304	ANEG 305	ANEG 306	ANEG 307	ANEG 308	ANEG 309	ANEG 310	ANEG 311	ANEG 312	ANEG 313	ANEG 314	ANEG 315	ANEG 316	ANEG 317	ANEG 318	ANEG 319	ANEG 320	ANEG 321	ANEG 322	ANEG 323	ANEG 324	ANEG 325	ANEG 326	ANEG 327	ANEG 328	ANEG 329	ANEG 330	ANEG 331	ANEG 332	ANEG 333	ANEG 334	ANEG 335	ANEG 336	ANEG 337	ANEG 338	ANEG 339	ANEG 340	ANEG 341	ANEG 342	ANEG 343	ANEG 344	ANEG 345	ANEG 346	ANEG 347	ANEG 348	ANEG 349	ANEG 350	ANEG 351	ANEG 352	ANEG 353	ANEG 354	ANEG 355	ANEG 356	ANEG 357	ANEG 358	ANEG 359	ANEG 360	ANEG 361	ANEG 362	ANEG 363	ANEG 364	ANEG 365	ANEG 366	ANEG 367	ANEG 368	ANEG 369	ANEG 370	ANEG 371	ANEG 372	ANEG 373	ANEG 374	ANEG 375	ANEG 376	ANEG 377	ANEG 378	ANEG 379	ANEG 380	ANEG 381	ANEG 382	ANEG 383	ANEG 384	ANEG 385	ANEG 386	ANEG 387	ANEG 388	ANEG 389	ANEG 390	ANEG 391	ANEG 392	ANEG 393	ANEG 394	ANEG 395	ANEG 396	ANEG 397	ANEG 398	ANEG 399	ANEG 400	ANEG 401	ANEG 402	ANEG 403	ANEG 404	ANEG 405	ANEG 406	ANEG 407	ANEG 408	ANEG 409	ANEG 410	ANEG 411	ANEG 412	ANEG 413	ANEG 414	ANEG 415	ANEG 416	ANEG 417	ANEG 418	ANEG 419	ANEG 420	ANEG 421	ANEG 422	ANEG 423	ANEG 424	ANEG 425	ANEG 426	ANEG 427	ANEG 428	ANEG 429	ANEG 430	ANEG 431	ANEG 432	ANEG 433	ANEG 434	ANEG 435	ANEG 436	ANEG 437	ANEG 438	ANEG 439	ANEG 440	ANEG 441	ANEG 442	ANEG 443	ANEG 444	ANEG 445	ANEG 446	ANEG 447	ANEG 448	ANEG 449	ANEG 450	ANEG 451	ANEG 452	ANEG 453	ANEG 454	ANEG 455	ANEG 456	ANEG 457	ANEG 458	ANEG 459	ANEG 460	ANEG 461	ANEG 462	ANEG 463	ANEG 464	ANEG 465	ANEG 466	ANEG 467	ANEG 468	ANEG 469	ANEG 470	ANEG 471	ANEG 472	ANEG 473	ANEG 474	ANEG 475	ANEG 476	ANEG 477	ANEG 478	ANEG 479	ANEG 480	ANEG 481	ANEG 482	ANEG 483	ANEG 484	ANEG 485	ANEG 486	ANEG 487	ANEG 488	ANEG 489	ANEG 490	ANEG 491	ANEG 492	ANEG 493	ANEG 494	ANEG 495	ANEG 496	ANEG 497	ANEG 498	ANEG 499	ANEG 500	ANEG 501	ANEG 502	ANEG 503	ANEG 504	ANEG 505	ANEG 506	ANEG 507	ANEG 508	ANEG 509	ANEG 510	ANEG 511	ANEG 512	ANEG 513	ANEG 514	ANEG 515	ANEG 516	ANEG 517	ANEG 518	ANEG 519	ANEG 520	ANEG 521	ANEG 522	ANEG 523	ANEG 524	ANEG 525	ANEG 526	ANEG 527	ANEG 528	ANEG 529	ANEG 530	ANEG 531	ANEG 532	ANEG 533	ANEG 534	ANEG 535	ANEG 536	ANEG 537	ANEG 538	ANEG 539	ANEG 540	ANEG 541	ANEG 542	ANEG 543	ANEG 544	ANEG 545	ANEG 546	ANEG 547	ANEG 548	ANEG 549	ANEG 550	ANEG 551	ANEG 552	ANEG 553	ANEG 554	ANEG 555	ANEG 556	ANEG 557	ANEG 558	ANEG 559	ANEG 560	ANEG 561	ANEG 562	ANEG 563	ANEG 564	ANEG 565	ANEG 566	ANEG 567	ANEG 568	ANEG 569	ANEG 570	ANEG 571	ANEG 572	ANEG 573	ANEG 574	ANEG 575	ANEG 576	ANEG 577	ANEG 578	ANEG 579	ANEG 580	ANEG 581	ANEG 582	ANEG 583	ANEG 584	ANEG 585	ANEG 586	ANEG 587	ANEG 588	ANEG 589	ANEG 590	ANEG 591	ANEG 592	ANEG 593	ANEG 594	ANEG 595	ANEG 596	ANEG 597	ANEG 598	ANEG 599	ANEG 600	ANEG 601	ANEG 602	ANEG 603	ANEG 604	ANEG 605	ANEG 606	ANEG 607	ANEG 608	ANEG 609	ANEG 610	ANEG 611	ANEG 612	ANEG 613	ANEG 614	ANEG 615	ANEG 616	ANEG 617	ANEG 618	ANEG 619	ANEG 620	ANEG 621	ANEG 622	ANEG 623	ANEG 624	ANEG 625	ANEG 626	ANEG 627	ANEG 628	ANEG 629	ANEG 630	ANEG 631	ANEG 632	ANEG 633	ANEG 634	ANEG 635	ANEG 636	ANEG 637	ANEG 638	ANEG 639	ANEG 640	ANEG 641	ANEG 642	ANEG 643	ANEG 644	ANEG 645	ANEG 646	ANEG 647	ANEG 648	ANEG 649	ANEG 650	ANEG 651	ANEG 652	ANEG 653	ANEG 654	ANEG 655	ANEG 656	ANEG 657	ANEG 658	ANEG 659	ANEG 660	ANEG 661	ANEG 662	ANEG 663	ANEG 664	ANEG 665	ANEG 666	ANEG 667	ANEG 668	ANEG 669	ANEG 670	ANEG 671	ANEG 672	ANEG 673	ANEG 674	ANEG 675	ANEG 676	ANEG 677	ANEG 678	ANEG 679	ANEG 680	ANEG 681	ANEG 682	ANEG 683	ANEG 684	ANEG 685	ANEG 686	ANEG 687	ANEG 688	ANEG 689	ANEG 690	ANEG 691	ANEG 692	ANEG 693	ANEG 694	ANEG 695	ANEG 696	ANEG 697	ANEG 698	ANEG 699	ANEG 700	ANEG 701	ANEG 702	ANEG 703	ANEG 704	ANEG 705	ANEG 706	ANEG 707	ANEG 708	ANEG 709	ANEG 710	ANEG 711	ANEG 712	ANEG 713	ANEG 714	ANEG 715	ANEG 716	ANEG 717	ANEG 718	ANEG 719	ANEG 720	ANEG 721	ANEG 722	ANEG 723	ANEG 724	ANEG 725	ANEG 726	ANEG 727	ANEG 728	ANEG 729	ANEG 730	ANEG 731	ANEG 732	ANEG 733	ANEG 734	ANEG 735	ANEG 736	ANEG 737	ANEG 738	ANEG 739	ANEG 740	ANEG 741	ANEG 742	ANEG 743	ANEG 744	ANEG 745	ANEG 746	ANEG 747	ANEG 748	ANEG 749	ANEG 750	ANEG 751	ANEG 752	ANEG 753	ANEG 754	ANEG 755	ANEG 756	ANEG 757	ANEG 758	ANEG 759	ANEG 760	ANEG 761	ANEG 762	ANEG 763	ANEG 764	ANEG 765	ANEG 766	ANEG 767	ANEG 768	ANEG 769	ANEG 770	ANEG 771	ANEG 772	ANEG 773	ANEG 774	ANEG 775	ANEG 776	ANEG 777	ANEG 778	ANEG 779	ANEG 780	ANEG 781	ANEG 782	ANEG 783	ANEG 784	ANEG 785	ANEG 786	ANEG 787	ANEG 788	ANEG 789	ANEG 790	ANEG 791	ANEG 792	ANEG 793	ANEG 794	ANEG 795	ANEG 796	ANEG 797	ANEG 798	ANEG 799	ANEG 800	ANEG 801	ANEG 802	ANEG 803	ANEG 804	ANEG 805	ANEG 806	ANEG 807	ANEG 808	ANEG 809	ANEG 810	ANEG 811	ANEG 812	ANEG 813	ANEG 814	ANEG 815	ANEG 816	ANEG 817	ANEG 818	ANEG 819	ANEG 820	ANEG 821	ANEG 822	ANEG 823	ANEG 824	ANEG 825	ANEG 826	ANEG 827	ANEG 828	ANEG 829	ANEG 830	ANEG 831	ANEG 832	ANEG 833	ANEG 834	ANEG 835	ANEG 836	ANEG 837	ANEG 838	ANEG 839	ANEG 840	ANEG 841	ANEG 842	ANEG 843	ANEG 844	ANEG 845	ANEG 846	ANEG 847	ANEG 848	ANEG 849	ANEG 850	ANEG 851	ANEG 852	ANEG 853	ANEG 854	ANEG 855	ANEG 856	ANEG 857	ANEG 858	ANEG 859	ANEG 860	ANEG 861	ANEG 862	ANEG 863	ANEG 864	ANEG 865	ANEG 866	ANEG 867	ANEG 868	ANEG 869	ANEG 870	ANEG 871	ANEG 872	ANEG 873	ANEG 874	ANEG 875	ANEG 876	ANEG 877	ANEG 878	ANEG 879	ANEG 880	ANEG 881	ANEG 882	ANEG 883	ANEG 884	ANEG 885	ANEG 886	ANEG 887	ANEG 888	ANEG 889	ANEG 890	ANEG 891	ANEG 892	ANEG 893	ANEG 894	ANEG 895	ANEG 896	ANEG 897	ANEG 898	ANEG 899	ANEG 900	ANEG 901	ANEG 902	ANEG 903	ANEG 904	ANEG 905	ANEG 906	ANEG 907	ANEG 908	ANEG 909	ANEG 910	ANEG 911	ANEG 912	ANEG 913	ANEG 914	ANEG 915	ANEG 916	ANEG 917	ANEG 918	ANEG 919	ANEG 920	ANEG 921	ANEG 922	ANEG 923	ANEG 924	ANEG 925	ANEG 926	ANEG 927	ANEG 928	ANEG 929	ANEG 930	ANEG 931	ANEG 932	ANEG 933	ANEG 934	ANEG 935	ANEG 936	ANEG 937	ANEG 938	ANEG 939	ANEG 940	ANEG 941	ANEG 942	ANEG 943	ANEG 944	ANEG 945	ANEG 946	ANEG 947	ANEG 948	ANEG 949	ANEG 950	ANEG 951	ANEG 952	ANEG 953	ANEG 954	ANEG 955	ANEG 956	ANEG 957	ANEG 958	ANEG 959	ANEG 960	ANEG 961	ANEG 962	ANEG 963	ANEG 964	ANEG 965	ANEG 966	ANEG 967	ANEG 968	ANEG 969	ANEG 970	ANEG 971	ANEG 972	ANEG 973	ANEG 974	ANEG 975	ANEG 976	ANEG 977	ANEG 978	ANEG 979	ANEG 980	ANEG 981	ANEG 982	ANEG 983	ANEG 984	ANEG 985	ANEG 986	ANEG 987	ANEG 988	ANEG 989	ANEG 990	ANEG 991	ANEG 992	ANEG 993	ANEG 994	ANEG 995	ANEG 996	ANEG 997	ANEG 998	ANEG 999	ANEG 1000
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170
Table 3 (cont'd)[illegible]

Table 3¹⁷¹ (cont'd)[illegible]

172
Table 3 (cont'd)[illegible]

Table 3 (cont'd)

Tissue	Thymus/lym	Thymus/lym	Thymus - 1a	Thymus node	Normal	Enrich	z	REG 001	YB05	z	REG 002	YB05	z	REG 003	YB05	z	REG 004	YB05	z	REG 005	YB05	z	REG 006	YB05	z	REG 007	YB05	z	REG 008	YB05	z	REG 009	YB05	z	REG 010	YB05	z	REG 011	YB05	z	REG 012	YB05	z	REG 013	YB05	z	REG 014	YB05	z	REG 015	YB05	z	REG 016	YB05	z	REG 017	YB05	z	REG 018	YB05	z	REG 019	YB05	z	REG 020	YB05	z	REG 021	YB05	z	REG 022	YB05	z	REG 023	YB05	z	REG 024	YB05	z	REG 025	YB05	z	REG 026	YB05	z	REG 027	YB05	z	REG 028	YB05	z	REG 029	YB05	z	REG 030	YB05	z	REG 031	YB05	z	REG 032	YB05	z	REG 033	YB05	z	REG 034	YB05	z	REG 035	YB05	z	REG 036	YB05	z	REG 037	YB05	z	REG 038	YB05	z	REG 039	YB05	z	REG 040	YB05	z	REG 041	YB05	z	REG 042	YB05	z	REG 043	YB05	z	REG 044	YB05	z	REG 045	YB05	z	REG 046	YB05	z	REG 047	YB05	z	REG 048	YB05	z	REG 049	YB05	z	REG 050	YB05	z	REG 051	YB05	z	REG 052	YB05	z	REG 053	YB05	z	REG 054	YB05	z	REG 055	YB05	z	REG 056	YB05	z	REG 057	YB05	z	REG 058	YB05	z	REG 059	YB05	z	REG 060	YB05	z	REG 061	YB05	z	REG 062	YB05	z	REG 063	YB05	z	REG 064	YB05	z	REG 065	YB05	z	REG 066	YB05	z	REG 067	YB05	z	REG 068	YB05	z	REG 069	YB05	z	REG 070	YB05	z	REG 071	YB05	z	REG 072	YB05	z	REG 073	YB05	z	REG 074	YB05	z	REG 075	YB05	z	REG 076	YB05	z	REG 077	YB05	z	REG 078	YB05	z	REG 079	YB05	z	REG 080	YB05	z	REG 081	YB05	z	REG 082	YB05	z	REG 083	YB05	z	REG 084	YB05	z	REG 085	YB05	z	REG 086	YB05	z	REG 087	YB05	z	REG 088	YB05	z	REG 089	YB05	z	REG 090	YB05	z	REG 091	YB05	z	REG 092	YB05	z	REG 093	YB05	z	REG 094	YB05	z	REG 095	YB05	z	REG 096	YB05	z	REG 097	YB05	z	REG 098	YB05	z	REG 099	YB05	z	REG 100	YB05	z	REG 101	YB05	z	REG 102	YB05	z	REG 103	YB05	z	REG 104	YB05	z	REG 105	YB05	z	REG 106	YB05	z	REG 107	YB05	z	REG 108	YB05	z	REG 109	YB05	z	REG 110	YB05	z	REG 111	YB05	z	REG 112	YB05	z	REG 113	YB05	z	REG 114	YB05	z	REG 115	YB05	z	REG 116	YB05	z	REG 117	YB05	z	REG 118	YB05	z	REG 119	YB05	z	REG 120	YB05	z	REG 121	YB05	z	REG 122	YB05	z	REG 123	YB05	z	REG 124	YB05	z	REG 125	YB05	z	REG 126	YB05	z	REG 127	YB05	z	REG 128	YB05	z	REG 129	YB05	z	REG 130	YB05	z	REG 131	YB05	z	REG 132	YB05	z	REG 133	YB05	z	REG 134	YB05	z	REG 135	YB05	z	REG 136	YB05	z	REG 137	YB05	z	REG 138	YB05	z	REG 139	YB05	z	REG 140	YB05	z	REG 141	YB05	z	REG 142	YB05	z	REG 143	YB05	z	REG 144	YB05	z	REG 145	YB05	z	REG 146	YB05	z	REG 147	YB05	z	REG 148	YB05	z	REG 149	YB05	z	REG 150	YB05	z	REG 151	YB05	z	REG 152	YB05	z	REG 153	YB05	z	REG 154	YB05	z	REG 155	YB05	z	REG 156	YB05	z	REG 157	YB05	z	REG 158	YB05	z	REG 159	YB05	z	REG 160	YB05	z	REG 161	YB05	z	REG 162	YB05	z	REG 163	YB05	z	REG 164	YB05	z	REG 165	YB05	z	REG 166	YB05	z	REG 167	YB05	z	REG 168	YB05	z	REG 169	YB05	z	REG 170	YB05	z	REG 171	YB05	z	REG 172	YB05	z	REG 173	YB05	z	REG 174	YB05	z	REG 175	YB05	z	REG 176	YB05	z	REG 177	YB05	z	REG 178	YB05	z	REG 179	YB05	z	REG 180	YB05	z	REG 181	YB05	z	REG 182	YB05	z	REG 183	YB05	z	REG 184	YB05	z	REG 185	YB05	z	REG 186	YB05	z	REG 187	YB05	z	REG 188	YB05	z	REG 189	YB05	z	REG 190	YB05	z	REG 191	YB05	z	REG 192	YB05	z	REG 193	YB05	z	REG 194	YB05	z	REG 195	YB05	z	REG 196	YB05	z	REG 197	YB05	z	REG 198	YB05	z	REG 199	YB05	z	REG 200	YB05	z	REG 201	YB05	z	REG 202	YB05	z	REG 203	YB05	z	REG 204	YB05	z	REG 205	YB05	z	REG 206	YB05	z	REG 207	YB05	z	REG 208	YB05	z	REG 209	YB05	z	REG 210	YB05	z	REG 211	YB05	z	REG 212	YB05	z	REG 213	YB05	z	REG 214	YB05	z	REG 215	YB05	z	REG 216	YB05	z	REG 217	YB05	z	REG 218	YB05	z	REG 219	YB05	z	REG 220	YB05	z	REG 221	YB05	z	REG 222	YB05	z	REG 223	YB05	z	REG 224	YB05	z	REG 225	YB05	z	REG 226	YB05	z	REG 227	YB05	z	REG 228	YB05	z	REG 229	YB05	z	REG 230	YB05	z	REG 231	YB05	z	REG 232	YB05	z	REG 233	YB05	z	REG 234	YB05	z	REG 235	YB05	z	REG 236	YB05	z	REG 237	YB05	z	REG 238	YB05	z	REG 239	YB05	z	REG 240	YB05	z	REG 241	YB05	z	REG 242	YB05	z	REG 243	YB05	z	REG 244	YB05	z	REG 245	YB05	z	REG 246	YB05	z	REG 247	YB05	z	REG 248	YB05	z	REG 249	YB05	z	REG 250	YB05	z	REG 251	YB05	z	REG 252	YB05	z	REG 253	YB05	z	REG 254	YB05	z	REG 255	YB05	z	REG 256	YB05	z	REG 257	YB05	z	REG 258	YB05	z	REG 259	YB05	z	REG 260	YB05	z	REG 261	YB05	z	REG 262	YB05	z	REG 263	YB05	z	REG 264	YB05	z	REG 265	YB05	z	REG 266	YB05	z	REG 267	YB05	z	REG 268	YB05	z	REG 269	YB05	z	REG 270	YB05	z	REG 271	YB05	z	REG 272	YB05	z	REG 273	YB05	z	REG 274	YB05	z	REG 275	YB05	z	REG 276	YB05	z	REG 277	YB05	z	REG 278	YB05	z	REG 279	YB05	z	REG 280	YB05	z	REG 281	YB05	z	REG 282	YB05	z	REG 283	YB05	z	REG 284	YB05	z	REG 285	YB05	z	REG 286	YB05	z	REG 287	YB05	z	REG 288	YB05	z	REG 289	YB05	z	REG 290	YB05	z	REG 291	YB05	z	REG 292	YB05	z	REG 293	YB05	z	REG 294	YB05	z	REG 295	YB05	z	REG 296	YB05	z	REG 297	YB05	z	REG 298	YB05	z	REG 299	YB05	z	REG 300	YB05	z	REG 301	YB05	z	REG 302	YB05	z	REG 303	YB05	z	REG 304	YB05	z	REG 305	YB05	z	REG 306	YB05	z	REG 307	YB05	z	REG 308	YB05	z	REG 309	YB05	z	REG 310	YB05	z	REG 311	YB05	z	REG 312	YB05	z	REG 313	YB05	z	REG 314	YB05	z	REG 315	YB05	z	REG 316	YB05	z	REG 317	YB05	z	REG 318	YB05	z	REG 319	YB05	z	REG 320	YB05	z	REG 321	YB05	z	REG 322	YB05	z	REG 323	YB05	z	REG 324	YB05	z	REG 325	YB05	z	REG 326	YB05	z	REG 327	YB05	z	REG 328	YB05	z	REG 329	YB05	z	REG 330	YB05	z	REG 331	YB05	z	REG 332	YB05	z	REG 333	YB05	z	REG 334	YB05	z	REG 335	YB05	z	REG 336	YB05	z	REG 337	YB05	z	REG 338	YB05	z	REG 339	YB05	z	REG 340	YB05	z	REG 341	YB05	z	REG 342	YB05	z	REG 343	YB05	z	REG 344	YB05	z	REG 345	YB05	z	REG 346	YB05	z	REG 347	YB05	z	REG 348	YB05	z	REG 349	YB05	z	REG 350	YB05	z	REG 351	YB05	z	REG 352	YB05	z	REG 353	YB05	z	REG 354	YB05	z	REG 355	YB05	z	REG 356	YB05	z	REG 357	YB05	z	REG 358	YB05	z	REG 359	YB05	z	REG 360	YB05	z	REG 361	YB05	z	REG 362	YB05	z	REG 363	YB05	z	REG 364	YB05	z	REG 365	YB05	z	REG 366	YB05	z	REG 367	YB05	z	REG 368	YB05	z	REG 369	YB05	z	REG 370	YB05	z	REG 371	YB05	z	REG 372	YB05	z	REG 373	YB05	z	REG 374	YB05	z	REG 375	YB05	z	REG 376	YB05	z	REG 377	YB05	z	REG 378	YB05	z	REG 379	YB05	z	REG 380	YB05	z	REG 381	YB05	z	REG 382	YB05	z	REG 383	YB05	z	REG 384	YB05	z	REG 385	YB05	z	REG 386	YB05	z	REG 387	YB05	z	REG 388	YB05	z	REG 389	YB05	z	REG 390	YB05	z	REG 391	YB05	z	REG 392	YB05	z	REG 393	YB05	z	REG 394	YB05	z	REG 395	YB05	z	REG 396	YB05	z	REG 397	YB05	z	REG 398	YB05	z	REG 399	YB05	z	REG 400	YB05	z	REG 401	YB05	z	REG 402	YB05	z	REG 403	YB05	z	REG 404	YB05	z	REG 405	YB05	z	REG 406	YB05	z	REG 407	YB05	z	REG 408	YB05	z	REG 409	YB05	z	REG 410	YB05	z	REG 411	YB05	z	REG 412	YB05	z	REG 413	YB05	z	REG 414	YB05	z	REG 415	YB05	z	REG 416	YB05	z	REG 417	YB05	z	REG 418	YB05	z	REG 419	YB05	z	REG 420	YB05	z	REG 421	YB05	z	REG 422	YB05	z	REG 423	YB05	z	REG 424	YB05	z	REG 425	YB05	z	REG 426	YB05	z	REG 427	YB05	z	REG 428	YB05	z	REG 429	YB05	z	REG 430	YB05	z	REG 431	YB05	z	REG 432	YB05	z	REG 433	YB05	z	REG 434	YB05	z	REG 435	YB05	z	REG 436	YB05	z	REG 437	YB05	z	REG 438	YB05	z	REG 439	YB05	z	REG 440	YB05	z	REG 441	YB05	z	REG 442	YB05	z	REG 443	YB05	z	REG 444	YB05	z	REG 445	YB05	z	REG 446	YB05	z	REG 447	YB05	z	REG 448	YB05	z	REG 449	YB05	z	REG 450	YB05	z	REG 451	YB05	z	REG 452	YB05	z	REG 453	YB05	z	REG 454	YB05	z	REG 455	YB05	z	REG 456	YB05	z	REG 457	YB05	z	REG 458	YB05	z	REG 459	YB05	z	REG 460	YB05	z	REG 461	YB05	z	REG 462	YB05	z	REG 463	YB05	z	REG 464	YB05	z	REG 465	YB05	z	REG 466	YB05	z	REG 467	YB05	z	REG 468	YB05	z	REG 469	YB05	z	REG 470	YB05	z	REG 471	YB05	z	REG 472	YB05	z	REG 473	YB05	z	REG 474	YB05	z	REG 475	YB05	z	REG 476	YB05	z	REG 477	YB05	z	REG 478	YB05	z	REG 479	YB05	z	REG 480	YB05	z	REG 481	YB05	z	REG 482	YB05	z	REG 483	YB05	z	REG 484	YB05	z	REG 485	YB05	z	REG 486	YB05	z	REG 487	YB05	z	REG 488	YB05	z	REG 489	YB05	z	REG 490	YB05	z	REG 491	YB05	z	REG 492	YB05	z	REG 493	
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174
Table 3 (cont'd)[illegible]

[illegible]

176
Table 3 (cont'd)[illegible]

177
Table 3 (cont'd)

Feature	Feature Sym	Intermediary	Turner - to	Turner - via	Normal	Ends	ps3	ISG 04	ANSEQ 05	WSEQ 06	ANSEQ 07	MESEQ 08	CSSEQ 09	MSSEQ 10	WSEQ 11	MSSEQ 12	ANSEQ 13
NAZVY	153							41443	847	10881	3442	20781	2887	8395	10873		
NAZVY	153							2729	1517	3252	2811	448	22251	1884	28821		
NAZVY	153							2886	38895	192	1902	2844	11880	3485	22310	81758	
NAZVY	153							778	18793	0	704	437	2890	4021	88458		
NAZVY	153							198	14878	1834	7208	183	8827	2185	17873	81728	
NAZVY	153							850	1518	0	1446	4	8452	1088	4201	81728	
NAZVY	153							40	12814	4858	877	1770	1071	2880	105881		
NAZVY	153							448	8459	1778	824	88	14004	2432	3834	105881	
NAZVY	153							1182	27353	1084	1844	2859	13118	1213	8385	12911	
NAZVY	153							323	8127	8512	104	0	18811	1317	84	43588	
NAZVY	153							1887	14486	3021	794	1827	7349	1878	7479	82871	
NAZVY	153							740	12215	771	857	889	4827	2887	7421	71188	
NAZVY	153							1723	28349	2549	2081	2853	10272	3331	7251	72587	
NAZVY	153							2684	8180	2708	439	1843	13401	1881	2407	86112	
NAZVY	153							303	37237	282	3101	4339	28232	882	8081	33734	
NAZVY	153							620	8811	0	1807	1839	10131	1195	2786	28388	
NAZVY	153							445	8427	1817	1828	1083	23880	1771	11881	12220	
NAZVY	153							1018	7208	0	148	413	11784	2012	1488	28888	
NAZVY	153							686	8219	827	1182	847	28889	1670	7153	11882	
NAZVY	153							1700	8889	0	387	1113	3812	1884	3255	71888	
NAZVY	153							810	8038	1428	1782	841	21777	1488	7225	82888	
NAZVY	153							377	10303	0	33	808	14288	1480	3181	48878	
NAZVY	153							1087	10222	1808	4327	377	20888	1884	13035	42881	
NAZVY	153							1200	8043	180	148	114	8882	2174	3888	48888	
NAZVY	153							881	10881	181	2088	334	48888	1833	18423	42879	
NAZVY	153							0	8783	0	1088	337	1784	2308	4070	44877	
NAZVY	153							8313	10889	211	288	0	14128	2478	10888	18881	
NAZVY	153							0	1223	0	2882	134	8784	2447	10871	78888	
NAZVY	153							288	4811	841	1184	242	1354	2057	2880	58834	
NAZVY	153							278	4888	2178	851	811	8881	1313	712	78888	
NAZVY	153							183	10843	8213	2442	877	3888	3828	4084	88888	
NAZVY	153							1044	4813	2234	380	588	8774	1771	8328	88888	
NAZVY	153							2174	13887	4184	242	1840	14318	1488	21344	48888	
NAZVY	153							1888	31773	588	4884	281	4881	1488	7228	18888	
NAZVY	153							845	6882	178	2448	188	1421	25044	42881	51888	
NAZVY	153							1112	7228	0	888	834	10017	1847	4888	41878	
NAZVY	153							0	8280	2082	8284	887	18788	888	24881	28887	
NAZVY	153							288	7284	384	1011	2778	8781	8781	18884	17888	
NAZVY	153							1271	14788	0	2748	2443	18288	13033	88888	51888	
NAZVY	153							1333	11809	0	8308	1084	18314	1080	8830	28888	
NAZVY	153							235	10129	1848	3385	1282	17882	2084	15885	42888	
NAZVY	153							1014	8882	1813	374	1811	2229	10888	18840	88888	
NAZVY	153							1081	11884	2328	8780	878	15224	1884	33438	40288	
NAZVY	153							252	7303	127	838	28	20030	1080	1880	40288	
NAZVY	153							2683	13887	3338	2812	473	11880	2188	28888	88888	
NAZVY	153							0	7485	8118	888	228	14888	2884	8128	50718	
NAZVY	153							822	18881	1882	2887	372	7883	4474	12488	10888	
NAZVY	153							0	10887	871	740	482	8184	2788	8282	81778	
NAZVY	153							872	12888	1798	5477	714	1781	2178	3888	54881	
NAZVY	153							0	10881	2031	288	685	2388	3272	7830	58878	
NAZVY	153							0	8485	888	3388	217	4083	2078	11182	42478	
NAZVY	153							247	7283	3432	887	874	8534	1848	4884	48888	
NAZVY	153							1114	10887	2887	782	12882	2885	31301	58888		
NAZVY	153							1508	4880	0	2538	218	28780	1814	8385	88888	
NAZVY	153							37	3414	0	477	80	28787	1484	10148	78829	
NAZVY	153							4783	10827	0	2880	784	11788	2188	5181	72818	
NAZVY	153							888	12483	88	20818	701	8828	2428	8414	41888	
NAZVY	153							0	2888	887	13214	0	1878	331	14888	18883	
NAZVY	153							0	2882	0	383	0	317	214	2447	10181	
NAZVY	153							0	2788	0	1888	0	232	187	218	18882	
NAZVY	153							0	4432	0	2172	0	888	242	15448	13882	
NAZVY	153							0	3418	0	878	0	1883	281	12280	20281	
NAZVY	153							0	2818	318	10488	0	2388	882	27454	14888	
NAZVY	153							0	8888	0	7440	0	2883	883	78184	18881	
NAZVY	153							0	4185	0	8532	0	1342	387	7118	18488	
NAZVY	153							0	2052	442	1804	0	2088	781	18882	27888	
NAZVY	153							0	8308	1804	88	0	1333	1388	8241	88888	
NAZVY	153							0	3484	0	2883	0	888	287	11222	18811	
NAZVY	153							0	4334	0	2219	0	177	321	18878	14247	
NAZVY	153							0	2871	882	287	0	707	181	18884	15888	
NAZVY	153							0	4888	0	3412	0	8	8	24887	14888	
NAZVY	153							0	2812	0	3411	0	388	118	8124	14350	
NAZVY	153							0	13125	0	4485	0	1125	880	44882	43272	
NAZVY	153							0	7888	208	1843	0	883	715	5378	15827	
NAZVY	153							0	3813	612	78	0	1841	828	25884	22888	
NAZVY	153							0	1814	0	8874	0	872	116	18218	11885	
NAZVY	153							0	8027	0	1818	0	838	310	4844	17885	
NAZVY	153							0	11054	172	1742	0	888	818	25884	21288	
NAZVY	153							0	8888	317	2812	0	2774	772	22788	13274	
NAZVY	153							0	8701	0	184	0	2280	785	25888	14200	
NAZVY	153							0	8553	0	1887	0	1877	780	8830	17161	
NAZVY	153							0	8181	887	888	0	1888	1033	12882	13288	
NAZVY	153							0	2872	1041	132	0	783	281	8888	13285	
NAZVY	153							0	8135	208	2880	0	208	888	18837	12311	
NAZVY	153							0	1882	787	1330	0	282	818	11288	10788	
NAZVY	153							0	8774	84	2888	0	2158	824	28287	18812	
NAZVY	153							0	8587	0	1084	0	1873	880	10878	18817	
NAZVY	153							0	8722	0	1828	0	488	788	13288	13828	
NAZVY	153							0	7888	0	2828	0	881	847	44884	12447	
NAZVY	153							0	11829	0	3883	0	1887	887	32308	18828	
NAZVY	153							0	3280	0	2040	0	1847	842	8878	17847	
NAZVY	153							0	8748	87	2847	0	888	234	18878	12714	
NAZVY	153							0	1778	0	7823	0	288	478	7747	14837	
NAZVY	153							0	4310	0	17881	0	888	384	16174	18888	
NAZVY	153							0	802	0	1151	0	1887	1882	13442	81832	

178.
Table 3 (cont'd)[illegible]

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Table 3 (cont'd)[illegible]

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Table 3 (cont'd)[illegible]

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Table 3 (cont'd)

Team	Team-yrn	Marsh-yrn	Turner - to	Turner early	Normal	Endless	ps3	SEQ 5	SEQ 6	SEQ 7	SEQ 8	SEQ 9	SEQ 10	SEQ 11	SEQ 12	SEQ 13	SEQ 14	SEQ 15	SEQ 16	SEQ 17	SEQ 18	SEQ 19	SEQ 20	SEQ 21	SEQ 22	SEQ 23	SEQ 24	SEQ 25	SEQ 26	SEQ 27	SEQ 28	SEQ 29	SEQ 30	SEQ 31	SEQ 32	SEQ 33	SEQ 34	SEQ 35	SEQ 36	SEQ 37	SEQ 38	SEQ 39	SEQ 40	SEQ 41	SEQ 42	SEQ 43	SEQ 44	SEQ 45	SEQ 46	SEQ 47	SEQ 48	SEQ 49	SEQ 50	SEQ 51	SEQ 52	SEQ 53	SEQ 54	SEQ 55	SEQ 56	SEQ 57	SEQ 58	SEQ 59	SEQ 60	SEQ 61	SEQ 62	SEQ 63	SEQ 64	SEQ 65	SEQ 66	SEQ 67	SEQ 68	SEQ 69	SEQ 70	SEQ 71	SEQ 72	SEQ 73	SEQ 74	SEQ 75	SEQ 76	SEQ 77	SEQ 78	SEQ 79	SEQ 80	SEQ 81	SEQ 82	SEQ 83	SEQ 84	SEQ 85	SEQ 86	SEQ 87	SEQ 88	SEQ 89	SEQ 90	SEQ 91	SEQ 92	SEQ 93	SEQ 94	SEQ 95	SEQ 96	SEQ 97	SEQ 98	SEQ 99	SEQ 100	SEQ 101	SEQ 102	SEQ 103	SEQ 104	SEQ 105	SEQ 106	SEQ 107	SEQ 108	SEQ 109	SEQ 110	SEQ 111	SEQ 112	SEQ 113	SEQ 114	SEQ 115	SEQ 116	SEQ 117	SEQ 118	SEQ 119	SEQ 120	SEQ 121	SEQ 122	SEQ 123	SEQ 124	SEQ 125	SEQ 126	SEQ 127	SEQ 128	SEQ 129	SEQ 130	SEQ 131	SEQ 132	SEQ 133	SEQ 134	SEQ 135	SEQ 136	SEQ 137	SEQ 138	SEQ 139	SEQ 140	SEQ 141	SEQ 142	SEQ 143	SEQ 144	SEQ 145	SEQ 146	SEQ 147	SEQ 148	SEQ 149	SEQ 150	SEQ 151	SEQ 152	SEQ 153	SEQ 154	SEQ 155	SEQ 156	SEQ 157	SEQ 158	SEQ 159	SEQ 160	SEQ 161	SEQ 162	SEQ 163	SEQ 164	SEQ 165	SEQ 166	SEQ 167	SEQ 168	SEQ 169	SEQ 170	SEQ 171	SEQ 172	SEQ 173	SEQ 174	SEQ 175	SEQ 176	SEQ 177	SEQ 178	SEQ 179	SEQ 180	SEQ 181	SEQ 182	SEQ 183	SEQ 184	SEQ 185	SEQ 186	SEQ 187	SEQ 188	SEQ 189	SEQ 190	SEQ 191	SEQ 192	SEQ 193	SEQ 194	SEQ 195	SEQ 196	SEQ 197	SEQ 198	SEQ 199	SEQ 200	SEQ 201	SEQ 202	SEQ 203	SEQ 204	SEQ 205	SEQ 206	SEQ 207	SEQ 208	SEQ 209	SEQ 210	SEQ 211	SEQ 212	SEQ 213	SEQ 214	SEQ 215	SEQ 216	SEQ 217	SEQ 218	SEQ 219	SEQ 220	SEQ 221	SEQ 222	SEQ 223	SEQ 224	SEQ 225	SEQ 226	SEQ 227	SEQ 228	SEQ 229	SEQ 230	SEQ 231	SEQ 232	SEQ 233	SEQ 234	SEQ 235	SEQ 236	SEQ 237	SEQ 238	SEQ 239	SEQ 240	SEQ 241	SEQ 242	SEQ 243	SEQ 244	SEQ 245	SEQ 246	SEQ 247	SEQ 248	SEQ 249	SEQ 250	SEQ 251	SEQ 252	SEQ 253	SEQ 254	SEQ 255	SEQ 256	SEQ 257	SEQ 258	SEQ 259	SEQ 260	SEQ 261	SEQ 262	SEQ 263	SEQ 264	SEQ 265	SEQ 266	SEQ 267	SEQ 268	SEQ 269	SEQ 270	SEQ 271	SEQ 272	SEQ 273	SEQ 274	SEQ 275	SEQ 276	SEQ 277	SEQ 278	SEQ 279	SEQ 280	SEQ 281	SEQ 282	SEQ 283	SEQ 284	SEQ 285	SEQ 286	SEQ 287	SEQ 288	SEQ 289	SEQ 290	SEQ 291	SEQ 292	SEQ 293	SEQ 294	SEQ 295	SEQ 296	SEQ 297	SEQ 298	SEQ 299	SEQ 300	SEQ 301	SEQ 302	SEQ 303	SEQ 304	SEQ 305	SEQ 306	SEQ 307	SEQ 308	SEQ 309	SEQ 310	SEQ 311	SEQ 312	SEQ 313	SEQ 314	SEQ 315	SEQ 316	SEQ 317	SEQ 318	SEQ 319	SEQ 320	SEQ 321	SEQ 322	SEQ 323	SEQ 324	SEQ 325	SEQ 326	SEQ 327	SEQ 328	SEQ 329	SEQ 330	SEQ 331	SEQ 332	SEQ 333	SEQ 334	SEQ 335	SEQ 336	SEQ 337	SEQ 338	SEQ 339	SEQ 340	SEQ 341	SEQ 342	SEQ 343	SEQ 344	SEQ 345	SEQ 346	SEQ 347	SEQ 348	SEQ 349	SEQ 350	SEQ 351	SEQ 352	SEQ 353	SEQ 354	SEQ 355	SEQ 356	SEQ 357	SEQ 358	SEQ 359	SEQ 360	SEQ 361	SEQ 362	SEQ 363	SEQ 364	SEQ 365	SEQ 366	SEQ 367	SEQ 368	SEQ 369	SEQ 370	SEQ 371	SEQ 372	SEQ 373	SEQ 374	SEQ 375	SEQ 376	SEQ 377	SEQ 378	SEQ 379	SEQ 380	SEQ 381	SEQ 382	SEQ 383	SEQ 384	SEQ 385	SEQ 386	SEQ 387	SEQ 388	SEQ 389	SEQ 390	SEQ 391	SEQ 392	SEQ 393	SEQ 394	SEQ 395	SEQ 396	SEQ 397	SEQ 398	SEQ 399	SEQ 400	SEQ 401	SEQ 402	SEQ 403	SEQ 404	SEQ 405	SEQ 406	SEQ 407	SEQ 408	SEQ 409	SEQ 410	SEQ 411	SEQ 412	SEQ 413	SEQ 414	SEQ 415	SEQ 416	SEQ 417	SEQ 418	SEQ 419	SEQ 420	SEQ 421	SEQ 422	SEQ 423	SEQ 424	SEQ 425	SEQ 426	SEQ 427	SEQ 428	SEQ 429	SEQ 430	SEQ 431	SEQ 432	SEQ 433	SEQ 434	SEQ 435	SEQ 436	SEQ 437	SEQ 438	SEQ 439	SEQ 440	SEQ 441	SEQ 442	SEQ 443	SEQ 444	SEQ 445	SEQ 446	SEQ 447	SEQ 448	SEQ 449	SEQ 450	SEQ 451	SEQ 452	SEQ 453	SEQ 454	SEQ 455	SEQ 456	SEQ 457	SEQ 458	SEQ 459	SEQ 460	SEQ 461	SEQ 462	SEQ 463	SEQ 464	SEQ 465	SEQ 466	SEQ 467	SEQ 468	SEQ 469	SEQ 470	SEQ 471	SEQ 472	SEQ 473	SEQ 474	SEQ 475	SEQ 476	SEQ 477	SEQ 478	SEQ 479	SEQ 480	SEQ 481	SEQ 482	SEQ 483	SEQ 484	SEQ 485	SEQ 486	SEQ 487	SEQ 488	SEQ 489	SEQ 490	SEQ 491	SEQ 492	SEQ 493	SEQ 494	SEQ 495	SEQ 496	SEQ 497	SEQ 498	SEQ 499	SEQ 500	SEQ 501	SEQ 502	SEQ 503	SEQ 504	SEQ 505	SEQ 506	SEQ 507	SEQ 508	SEQ 509	SEQ 510	SEQ 511	SEQ 512	SEQ 513	SEQ 514	SEQ 515	SEQ 516	SEQ 517	SEQ 518	SEQ 519	SEQ 520	SEQ 521	SEQ 522	SEQ 523	SEQ 524	SEQ 525	SEQ 526	SEQ 527	SEQ 528	SEQ 529	SEQ 530	SEQ 531	SEQ 532	SEQ 533	SEQ 534	SEQ 535	SEQ 536	SEQ 537	SEQ 538	SEQ 539	SEQ 540	SEQ 541	SEQ 542	SEQ 543	SEQ 544	SEQ 545	SEQ 546	SEQ 547	SEQ 548	SEQ 549	SEQ 550	SEQ 551	SEQ 552	SEQ 553	SEQ 554	SEQ 555	SEQ 556	SEQ 557	SEQ 558	SEQ 559	SEQ 560	SEQ 561	SEQ 562	SEQ 563	SEQ 564	SEQ 565	SEQ 566	SEQ 567	SEQ 568	SEQ 569	SEQ 570	SEQ 571	SEQ 572	SEQ 573	SEQ 574	SEQ 575	SEQ 576	SEQ 577	SEQ 578	SEQ 579	SEQ 580	SEQ 581	SEQ 582	SEQ 583	SEQ 584	SEQ 585	SEQ 586	SEQ 587	SEQ 588	SEQ 589	SEQ 590	SEQ 591	SEQ 592	SEQ 593	SEQ 594	SEQ 595	SEQ 596	SEQ 597	SEQ 598	SEQ 599	SEQ 600	SEQ 601	SEQ 602	SEQ 603	SEQ 604	SEQ 605	SEQ 606	SEQ 607	SEQ 608	SEQ 609	SEQ 610	SEQ 611	SEQ 612	SEQ 613	SEQ 614	SEQ 615	SEQ 616	SEQ 617	SEQ 618	SEQ 619	SEQ 620	SEQ 621	SEQ 622	SEQ 623	SEQ 624	SEQ 625	SEQ 626	SEQ 627	SEQ 628	SEQ 629	SEQ 630	SEQ 631	SEQ 632	SEQ 633	SEQ 634	SEQ 635	SEQ 636	SEQ 637	SEQ 638	SEQ 639	SEQ 640	SEQ 641	SEQ 642	SEQ 643	SEQ 644	SEQ 645	SEQ 646	SEQ 647	SEQ 648	SEQ 649	SEQ 650	SEQ 651	SEQ 652	SEQ 653	SEQ 654	SEQ 655	SEQ 656	SEQ 657	SEQ 658	SEQ 659	SEQ 660	SEQ 661	SEQ 662	SEQ 663	SEQ 664	SEQ 665	SEQ 666	SEQ 667	SEQ 668	SEQ 669	SEQ 670	SEQ 671	SEQ 672	SEQ 673	SEQ 674	SEQ 675	SEQ 676	SEQ 677	SEQ 678	SEQ 679	SEQ 680	SEQ 681	SEQ 682	SEQ 683	SEQ 684	SEQ 685	SEQ 686	SEQ 687	SEQ 688	SEQ 689	SEQ 690	SEQ 691	SEQ 692	SEQ 693	SEQ 694	SEQ 695	SEQ 696	SEQ 697	SEQ 698	SEQ 699	SEQ 700	SEQ 701	SEQ 702	SEQ 703	SEQ 704	SEQ 705	SEQ 706	SEQ 707	SEQ 708	SEQ 709	SEQ 710	SEQ 711	SEQ 712	SEQ 713	SEQ 714	SEQ 715	SEQ 716	SEQ 717	SEQ 718	SEQ 719	SEQ 720	SEQ 721	SEQ 722	SEQ 723	SEQ 724	SEQ 725	SEQ 726	SEQ 727	SEQ 728	SEQ 729	SEQ 730	SEQ 731	SEQ 732	SEQ 733	SEQ 734	SEQ 735	SEQ 736	SEQ 737	SEQ 738	SEQ 739	SEQ 740	SEQ 741	SEQ 742	SEQ 743	SEQ 744	SEQ 745	SEQ 746	SEQ 747	SEQ 748	SEQ 749	SEQ 750	SEQ 751	SEQ 752	SEQ 753	SEQ 754	SEQ 755	SEQ 756	SEQ 757	SEQ 758	SEQ 759	SEQ 760	SEQ 761	SEQ 762	SEQ 763	SEQ 764	SEQ 765	SEQ 766	SEQ 767	SEQ 768	SEQ 769	SEQ 770	SEQ 771	SEQ 772	SEQ 773	SEQ 774	SEQ 775	SEQ 776	SEQ 777	SEQ 778	SEQ 779	SEQ 780	SEQ 781	SEQ 782	SEQ 783	SEQ 784	SEQ 785	SEQ 786	SEQ 787	SEQ 788	SEQ 789	SEQ 790	SEQ 791	SEQ 792	SEQ 793	SEQ 794	SEQ 795	SEQ 796	SEQ 797	SEQ 798	SEQ 799	SEQ 800	SEQ 801	SEQ 802	SEQ 803	SEQ 804	SEQ 805	SEQ 806	SEQ 807	SEQ 808	SEQ 809	SEQ 810	SEQ 811	SEQ 812	SEQ 813	SEQ 814	SEQ 815	SEQ 816	SEQ 817	SEQ 818	SEQ 819	SEQ 820	SEQ 821	SEQ 822	SEQ 823	SEQ 824	SEQ 825	SEQ 826	SEQ 827	SEQ 828	SEQ 829	SEQ 830	SEQ 831	SEQ 832	SEQ 833	SEQ 834	SEQ 835	SEQ 836	SEQ 837	SEQ 838	SEQ 839	SEQ 840	SEQ 841	SEQ 842	SEQ 843	SEQ 844	SEQ 845	SEQ 846	SEQ 847	SEQ 848	SEQ 849	SEQ 850	SEQ 851	SEQ 852	SEQ 853	SEQ 854	SEQ 855	SEQ 856	SEQ 857	SEQ 858	SEQ 859	SEQ 860	SEQ 861	SEQ 862	SEQ 863	SEQ 864	SEQ 865	SEQ 866	SEQ 867	SEQ 868	SEQ 869	SEQ 870	SEQ 871	SEQ 872	SEQ 873	SEQ 874	SEQ 875	SEQ 876	SEQ 877	SEQ 878	SEQ 879	SEQ 880	SEQ 881	SEQ 882	SEQ 883	SEQ 884	SEQ 885	SEQ 886	SEQ 887	SEQ 888	SEQ 889	SEQ 890	SEQ 891	SEQ 892	SEQ 893	SEQ 894	SEQ 895	SEQ 896	SEQ 897	SEQ 898	SEQ 899	SEQ 900	SEQ 901	SEQ 902	SEQ 903	SEQ 904	SEQ 905	SEQ 906	SEQ 907	SEQ 908	SEQ 909	SEQ 910	SEQ 911	SEQ 912	SEQ 913	SEQ 914	SEQ 915	SEQ 916	SEQ 917	SEQ 918	SEQ 919	SEQ 920	SEQ 921	SEQ 922	SEQ 923	SEQ 924	SEQ 925	SEQ 926	SEQ 927	SEQ 928	SEQ 929	SEQ 930	SEQ 931	SEQ 932	SEQ 933	SEQ 934	SEQ 935	SEQ 936	SEQ 937	SEQ 938	SEQ 939	SEQ 940	SEQ 941	SEQ 942	SEQ 943	SEQ 944	SEQ 945	SEQ 946	SEQ 947	SEQ 948	SEQ 949	SEQ 950	SEQ 951	SEQ 952	SEQ 953	SEQ 954	SEQ 955	SEQ 956	SEQ 957	SEQ 958	SEQ 959	SEQ 960	SEQ 961	SEQ 962	SEQ 963	SEQ 964	SEQ 965	SEQ 966	SEQ 967	SEQ 968	SEQ 969	SEQ 970	SEQ 971	SEQ 972	SEQ 973	SEQ 974	SEQ 975	SEQ 976	SEQ 977	SEQ 978	SEQ 979	SEQ 980	SEQ 981	SEQ 982	SEQ 983	SEQ 984	SEQ 985	SEQ 986	SEQ 987	SEQ 988	SEQ 989	SEQ 990	SEQ 991	SEQ 992	SEQ 993	SEQ 994	SEQ 995	SEQ 996	SEQ 997	SEQ 998	SEQ 999	SEQ 1000
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184
Table 3 (cont'd)

Gene	Yeast-yeast	Human-yeast	Yeast - to	Yeast cells	Human	Ends	AS	SEQ 55 AS260 54	SEQ 57	SEQ 58	SEQ 59	SEQ 60	SEQ 61	SEQ 62	SEQ 63	SEQ 64	SEQ 65	SEQ 66	SEQ 67	SEQ 68	SEQ 69	SEQ 70	SEQ 71	SEQ 72	SEQ 73	SEQ 74	SEQ 75	SEQ 76	SEQ 77	SEQ 78	SEQ 79	SEQ 80	SEQ 81	SEQ 82	SEQ 83	SEQ 84	SEQ 85	SEQ 86	SEQ 87	SEQ 88	SEQ 89	SEQ 90	SEQ 91	SEQ 92	SEQ 93	SEQ 94	SEQ 95	SEQ 96	SEQ 97	SEQ 98	SEQ 99	SEQ 100	SEQ 101	SEQ 102	SEQ 103	SEQ 104	SEQ 105	SEQ 106	SEQ 107	SEQ 108	SEQ 109	SEQ 110	SEQ 111	SEQ 112	SEQ 113	SEQ 114	SEQ 115	SEQ 116	SEQ 117	SEQ 118	SEQ 119	SEQ 120	SEQ 121	SEQ 122	SEQ 123	SEQ 124	SEQ 125	SEQ 126	SEQ 127	SEQ 128	SEQ 129	SEQ 130	SEQ 131	SEQ 132	SEQ 133	SEQ 134	SEQ 135	SEQ 136	SEQ 137	SEQ 138	SEQ 139	SEQ 140	SEQ 141	SEQ 142	SEQ 143	SEQ 144	SEQ 145	SEQ 146	SEQ 147	SEQ 148	SEQ 149	SEQ 150	SEQ 151	SEQ 152	SEQ 153	SEQ 154	SEQ 155	SEQ 156	SEQ 157	SEQ 158	SEQ 159	SEQ 160	SEQ 161	SEQ 162	SEQ 163	SEQ 164	SEQ 165	SEQ 166	SEQ 167	SEQ 168	SEQ 169	SEQ 170	SEQ 171	SEQ 172	SEQ 173	SEQ 174	SEQ 175	SEQ 176	SEQ 177	SEQ 178	SEQ 179	SEQ 180	SEQ 181	SEQ 182	SEQ 183	SEQ 184	SEQ 185	SEQ 186	SEQ 187	SEQ 188	SEQ 189	SEQ 190	SEQ 191	SEQ 192	SEQ 193	SEQ 194	SEQ 195	SEQ 196	SEQ 197	SEQ 198	SEQ 199	SEQ 200	SEQ 201	SEQ 202	SEQ 203	SEQ 204	SEQ 205	SEQ 206	SEQ 207	SEQ 208	SEQ 209	SEQ 210	SEQ 211	SEQ 212	SEQ 213	SEQ 214	SEQ 215	SEQ 216	SEQ 217	SEQ 218	SEQ 219	SEQ 220	SEQ 221	SEQ 222	SEQ 223	SEQ 224	SEQ 225	SEQ 226	SEQ 227	SEQ 228	SEQ 229	SEQ 230	SEQ 231	SEQ 232	SEQ 233	SEQ 234	SEQ 235	SEQ 236	SEQ 237	SEQ 238	SEQ 239	SEQ 240	SEQ 241	SEQ 242	SEQ 243	SEQ 244	SEQ 245	SEQ 246	SEQ 247	SEQ 248	SEQ 249	SEQ 250	SEQ 251	SEQ 252	SEQ 253	SEQ 254	SEQ 255	SEQ 256	SEQ 257	SEQ 258	SEQ 259	SEQ 260	SEQ 261	SEQ 262	SEQ 263	SEQ 264	SEQ 265	SEQ 266	SEQ 267	SEQ 268	SEQ 269	SEQ 270	SEQ 271	SEQ 272	SEQ 273	SEQ 274	SEQ 275	SEQ 276	SEQ 277	SEQ 278	SEQ 279	SEQ 280	SEQ 281	SEQ 282	SEQ 283	SEQ 284	SEQ 285	SEQ 286	SEQ 287	SEQ 288	SEQ 289	SEQ 290	SEQ 291	SEQ 292	SEQ 293	SEQ 294	SEQ 295	SEQ 296	SEQ 297	SEQ 298	SEQ 299	SEQ 300	SEQ 301	SEQ 302	SEQ 303	SEQ 304	SEQ 305	SEQ 306	SEQ 307	SEQ 308	SEQ 309	SEQ 310	SEQ 311	SEQ 312	SEQ 313	SEQ 314	SEQ 315	SEQ 316	SEQ 317	SEQ 318	SEQ 319	SEQ 320	SEQ 321	SEQ 322	SEQ 323	SEQ 324	SEQ 325	SEQ 326	SEQ 327	SEQ 328	SEQ 329	SEQ 330	SEQ 331	SEQ 332	SEQ 333	SEQ 334	SEQ 335	SEQ 336	SEQ 337	SEQ 338	SEQ 339	SEQ 340	SEQ 341	SEQ 342	SEQ 343	SEQ 344	SEQ 345	SEQ 346	SEQ 347	SEQ 348	SEQ 349	SEQ 350	SEQ 351	SEQ 352	SEQ 353	SEQ 354	SEQ 355	SEQ 356	SEQ 357	SEQ 358	SEQ 359	SEQ 360	SEQ 361	SEQ 362	SEQ 363	SEQ 364	SEQ 365	SEQ 366	SEQ 367	SEQ 368	SEQ 369	SEQ 370	SEQ 371	SEQ 372	SEQ 373	SEQ 374	SEQ 375	SEQ 376	SEQ 377	SEQ 378	SEQ 379	SEQ 380	SEQ 381	SEQ 382	SEQ 383	SEQ 384	SEQ 385	SEQ 386	SEQ 387	SEQ 388	SEQ 389	SEQ 390	SEQ 391	SEQ 392	SEQ 393	SEQ 394	SEQ 395	SEQ 396	SEQ 397	SEQ 398	SEQ 399	SEQ 400	SEQ 401	SEQ 402	SEQ 403	SEQ 404	SEQ 405	SEQ 406	SEQ 407	SEQ 408	SEQ 409	SEQ 410	SEQ 411	SEQ 412	SEQ 413	SEQ 414	SEQ 415	SEQ 416	SEQ 417	SEQ 418	SEQ 419	SEQ 420	SEQ 421	SEQ 422	SEQ 423	SEQ 424	SEQ 425	SEQ 426	SEQ 427	SEQ 428	SEQ 429	SEQ 430	SEQ 431	SEQ 432	SEQ 433	SEQ 434	SEQ 435	SEQ 436	SEQ 437	SEQ 438	SEQ 439	SEQ 440	SEQ 441	SEQ 442	SEQ 443	SEQ 444	SEQ 445	SEQ 446	SEQ 447	SEQ 448	SEQ 449	SEQ 450	SEQ 451	SEQ 452	SEQ 453	SEQ 454	SEQ 455	SEQ 456	SEQ 457	SEQ 458	SEQ 459	SEQ 460	SEQ 461	SEQ 462	SEQ 463	SEQ 464	SEQ 465	SEQ 466	SEQ 467	SEQ 468	SEQ 469	SEQ 470	SEQ 471	SEQ 472	SEQ 473	SEQ 474	SEQ 475	SEQ 476	SEQ 477	SEQ 478	SEQ 479	SEQ 480	SEQ 481	SEQ 482	SEQ 483	SEQ 484	SEQ 485	SEQ 486	SEQ 487	SEQ 488	SEQ 489	SEQ 490	SEQ 491	SEQ 492	SEQ 493	SEQ 494	SEQ 495	SEQ 496	SEQ 497	SEQ 498	SEQ 499	SEQ 500	SEQ 501	SEQ 502	SEQ 503	SEQ 504	SEQ 505	SEQ 506	SEQ 507	SEQ 508	SEQ 509	SEQ 510	SEQ 511	SEQ 512	SEQ 513	SEQ 514	SEQ 515	SEQ 516	SEQ 517	SEQ 518	SEQ 519	SEQ 520	SEQ 521	SEQ 522	SEQ 523	SEQ 524	SEQ 525	SEQ 526	SEQ 527	SEQ 528	SEQ 529	SEQ 530	SEQ 531	SEQ 532	SEQ 533	SEQ 534	SEQ 535	SEQ 536	SEQ 537	SEQ 538	SEQ 539	SEQ 540	SEQ 541	SEQ 542	SEQ 543	SEQ 544	SEQ 545	SEQ 546	SEQ 547	SEQ 548	SEQ 549	SEQ 550	SEQ 551	SEQ 552	SEQ 553	SEQ 554	SEQ 555	SEQ 556	SEQ 557	SEQ 558	SEQ 559	SEQ 560	SEQ 561	SEQ 562	SEQ 563	SEQ 564	SEQ 565	SEQ 566	SEQ 567	SEQ 568	SEQ 569	SEQ 570	SEQ 571	SEQ 572	SEQ 573	SEQ 574	SEQ 575	SEQ 576	SEQ 577	SEQ 578	SEQ 579	SEQ 580	SEQ 581	SEQ 582	SEQ 583	SEQ 584	SEQ 585	SEQ 586	SEQ 587	SEQ 588	SEQ 589	SEQ 590	SEQ 591	SEQ 592	SEQ 593	SEQ 594	SEQ 595	SEQ 596	SEQ 597	SEQ 598	SEQ 599	SEQ 600	SEQ 601	SEQ 602	SEQ 603	SEQ 604	SEQ 605	SEQ 606	SEQ 607	SEQ 608	SEQ 609	SEQ 610	SEQ 611	SEQ 612	SEQ 613	SEQ 614	SEQ 615	SEQ 616	SEQ 617	SEQ 618	SEQ 619	SEQ 620	SEQ 621	SEQ 622	SEQ 623	SEQ 624	SEQ 625	SEQ 626	SEQ 627	SEQ 628	SEQ 629	SEQ 630	SEQ 631	SEQ 632	SEQ 633	SEQ 634	SEQ 635	SEQ 636	SEQ 637	SEQ 638	SEQ 639	SEQ 640	SEQ 641	SEQ 642	SEQ 643	SEQ 644	SEQ 645	SEQ 646	SEQ 647	SEQ 648	SEQ 649	SEQ 650	SEQ 651	SEQ 652	SEQ 653	SEQ 654	SEQ 655	SEQ 656	SEQ 657	SEQ 658	SEQ 659	SEQ 660	SEQ 661	SEQ 662	SEQ 663	SEQ 664	SEQ 665	SEQ 666	SEQ 667	SEQ 668	SEQ 669	SEQ 670	SEQ 671	SEQ 672	SEQ 673	SEQ 674	SEQ 675	SEQ 676	SEQ 677	SEQ 678	SEQ 679	SEQ 680	SEQ 681	SEQ 682	SEQ 683	SEQ 684	SEQ 685	SEQ 686	SEQ 687	SEQ 688	SEQ 689	SEQ 690	SEQ 691	SEQ 692	SEQ 693	SEQ 694	SEQ 695	SEQ 696	SEQ 697	SEQ 698	SEQ 699	SEQ 700	SEQ 701	SEQ 702	SEQ 703	SEQ 704	SEQ 705	SEQ 706	SEQ 707	SEQ 708	SEQ 709	SEQ 710	SEQ 711	SEQ 712	SEQ 713	SEQ 714	SEQ 715	SEQ 716	SEQ 717	SEQ 718	SEQ 719	SEQ 720	SEQ 721	SEQ 722	SEQ 723	SEQ 724	SEQ 725	SEQ 726	SEQ 727	SEQ 728	SEQ 729	SEQ 730	SEQ 731	SEQ 732	SEQ 733	SEQ 734	SEQ 735	SEQ 736	SEQ 737	SEQ 738	SEQ 739	SEQ 740	SEQ 741	SEQ 742	SEQ 743	SEQ 744	SEQ 745	SEQ 746	SEQ 747	SEQ 748	SEQ 749	SEQ 750	SEQ 751	SEQ 752	SEQ 753	SEQ 754	SEQ 755	SEQ 756	SEQ 757	SEQ 758	SEQ 759	SEQ 760	SEQ 761	SEQ 762	SEQ 763	SEQ 764	SEQ 765	SEQ 766	SEQ 767	SEQ 768	SEQ 769	SEQ 770	SEQ 771	SEQ 772	SEQ 773	SEQ 774	SEQ 775	SEQ 776	SEQ 777	SEQ 778	SEQ 779	SEQ 780	SEQ 781	SEQ 782	SEQ 783	SEQ 784	SEQ 785	SEQ 786	SEQ 787	SEQ 788	SEQ 789	SEQ 790	SEQ 791	SEQ 792	SEQ 793	SEQ 794	SEQ 795	SEQ 796	SEQ 797	SEQ 798	SEQ 799	SEQ 800	SEQ 801	SEQ 802	SEQ 803	SEQ 804	SEQ 805	SEQ 806	SEQ 807	SEQ 808	SEQ 809	SEQ 810	SEQ 811	SEQ 812	SEQ 813	SEQ 814	SEQ 815	SEQ 816	SEQ 817	SEQ 818	SEQ 819	SEQ 820	SEQ 821	SEQ 822	SEQ 823	SEQ 824	SEQ 825	SEQ 826	SEQ 827	SEQ 828	SEQ 829	SEQ 830	SEQ 831	SEQ 832	SEQ 833	SEQ 834	SEQ 835	SEQ 836	SEQ 837	SEQ 838	SEQ 839	SEQ 840	SEQ 841	SEQ 842	SEQ 843	SEQ 844	SEQ 845	SEQ 846	SEQ 847	SEQ 848	SEQ 849	SEQ 850	SEQ 851	SEQ 852	SEQ 853	SEQ 854	SEQ 855	SEQ 856	SEQ 857	SEQ 858	SEQ 859	SEQ 860	SEQ 861	SEQ 862	SEQ 863	SEQ 864	SEQ 865	SEQ 866	SEQ 867	SEQ 868	SEQ 869	SEQ 870	SEQ 871	SEQ 872	SEQ 873	SEQ 874	SEQ 875	SEQ 876	SEQ 877	SEQ 878	SEQ 879	SEQ 880	SEQ 881	SEQ 882	SEQ 883	SEQ 884	SEQ 885	SEQ 886	SEQ 887	SEQ 888	SEQ 889	SEQ 890	SEQ 891	SEQ 892	SEQ 893	SEQ 894	SEQ 895	SEQ 896	SEQ 897	SEQ 898	SEQ 899	SEQ 900	SEQ 901	SEQ 902	SEQ 903	SEQ 904	SEQ 905	SEQ 906	SEQ 907	SEQ 908	SEQ 909	SEQ 910	SEQ 911	SEQ 912	SEQ 913	SEQ 914	SEQ 915	SEQ 916	SEQ 917	SEQ 918	SEQ 919	SEQ 920	SEQ 921	SEQ 922	SEQ 923	SEQ 924	SEQ 925	SEQ 926	SEQ 927	SEQ 928	SEQ 929	SEQ 930	SEQ 931	SEQ 932	SEQ 933	SEQ 934	SEQ 935	SEQ 936	SEQ 937	SEQ 938	SEQ 939	SEQ 940	SEQ 941	SEQ 942	SEQ 943	SEQ 944	SEQ 945	SEQ 946	SEQ 947	SEQ 948	SEQ 949	SEQ 950	SEQ 951	SEQ 952	SEQ 953	SEQ 954	SEQ 955	SEQ 956	SEQ 957	SEQ 958	SEQ 959	SEQ 960	SEQ 961	SEQ 962	SEQ 963	SEQ 964	SEQ 965	SEQ 966	SEQ 967	SEQ 968	SEQ 969	SEQ 970	SEQ 971	SEQ 972	SEQ 973	SEQ 974	SEQ 975	SEQ 976	SEQ 977	SEQ 978	SEQ 979	SEQ 980	SEQ 981	SEQ 982	SEQ 983	SEQ 984	SEQ 985	SEQ 986	SEQ 987	SEQ 988	SEQ 989	SEQ 990	SEQ 991	SEQ 992	SEQ 993	SEQ 994	SEQ 995	SEQ 996	SEQ 997	SEQ 998	SEQ 999	SEQ 1000
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Table 3 (contd)

[illegible]

[illegible]

Table 3 (cont'd)

Table 3 (cont'd)

Tumor	Tumor-prim	Normal-prim	Tumor - 1e	Tumor cells	Normal	Endos	p53	SEQ ID NO
2A-FX1	155							0
MCF-TMOR-RES	153							0
MCF-7	151							0
M14	149							0
UACC-353	147							22
UACC-82	145							0
SK-MEL-70	144							23
UO-31	143							0
SK-MEL-5	142							81
RM-12	141							4
SK-MEL-2	140							265
HCT-116	139							239
UACC-3M	138							181
COLO 205	137							290
LOX-BAT	136							0
SW-620	135							0
TK-18	134							0
HCT-118	133							0
786-O	132							92
MCC-2008	131							79
ACHN	130							279
PC-3	129							0
QGP-263	128							268
DU-145	127							89
C8-1	126							279
BR	125							0
A498	124							127
COX2-RES	123							0
EW12C	122							120
H6-40	121							0
MOL-74	120							114
QVCAR-5	119							0
K-562	118							36
QVCAR-4	117							842
QVCAR-3M	116							89
QVCAR-3	115							181
SP-538	114							87
MOP-62	113							0
SC-293	112							181
LA-MET-CC	111							110
SP-202	110							135
HCT-1162	109							0
1251	108							304
MCF-H200	107							0
SMB-78	106							36
MCF-H200M	105							430
SMB-18	104							78
MCF-H200	103							82
SK-OV-3	102							0
MCF-102	101							777
MDAMB-231	100							0
SK-VX	99							84
QVCAR-4	98							8
MCF-62	97							43
h. Bcr/Abi auto 321/82 #12	49							148
h. Bcr/Abi auto 102/192 #17	47							210
h. Bcr/Abi auto 225/52 #13	46							135
TCOP	45							0
AS49-1						wt		0
AS49-2						wt		375
AS49-3						wt		458
AS49-5						wt		267
AS49-7						wt		72
SK-VX-1						mutant		84
SK-VX-4						mutant		390
SK-VX-3						mutant		0
SK-VX-6						mutant		463
SK-VX-7						mutant		877
SK-VX-1						wt		0
MCF-7-3						wt		805
MCF-7-4						wt		218
MCF-7-5						wt		0
MCF-7-7						wt		0
ADR-RES-1						mutant		3049
ADR-RES-2						mutant		159
ADR-RES-4						mutant		79
ADR-RES-5						mutant		18
ADR-RES-7						wt		95
WI-38-1						wt		283
WI-38-2						wt		680
WI-38-4						wt		680
WI-38-5						wt		83
WI-38-7						wt		0
HLA-1						HPV E6		0
HLA-2						HPV E6		86
HLA-4						HPV E6		185
HLA-5						HPV E6		308
HLA-7						HPV E6		105
H1299-1						mutant		0
H1299-2						mutant		0
H1299-4						mutant		0
H1299-5						mutant		0
H1299-7						mutant		1
AS49-8						wt		193
SK-VX-2						mutant		8
HCT-116-1						wt		0
HCT-116-2						mutant		805
HT29-3						mutant		88
SP630-1						wt		0
SP630-2						mutant		208
SP-305-1						mutant		631
SP-305-2						wt		0
QVCAR-4-1						wt		0
QVCAR-4-2						wt		0
QVCAR-5-1						mutant		820
QVCAR-5-2						mutant		208
MCF-7-2						wt		86
ADR-RES-2						mutant		231
TM4-2						HPV E6		172
SW-620-1						mutant		0
SW-620-2						mutant		191
H1299-2						mutant		1005
C33A-1						mutant		0
C33A-2						mutant		0
LOX-1						mutant		271
LOX-2						mutant		977
Hep2-1						wt		0
Hep2-2						wt		24
WI-38-2						wt		295
Mam-1						wt		0
Mam-2						wt		0
Mam-3						wt		0
Mam-4						wt		14520
Mam-5						wt		537
Mam-6						wt		0
Mam-7						wt		0
Mam-8						wt		0

190
Table 3 (cont'd)

[illegible]

Table 4

Gene Name	SP ID#	na ID#	aa	Family	Group	Length_AA	Extra-Catalytic Domains (Amino acid positions)
X69117 h beta_adrenergic	H	1	122	AGC	GRK	688	Regulator of G protein signaling domain 54-175; PH domain 559-652
AA144574 m	M	2	123	AGC	GRK	378	PH domain 249-337
AA210825 h	H	9	130	AGC	PKC	978	Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577
AA316804 h	H	11	132	AGC	PKC	890	Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532
AA887783 h	H	21	142	AGC	SGK	446	PX domain 13-120
AA021445 h 3	H	32	152	CAMK	EMK	1311	Vitamin K-dependent carboxylation/gamma-carboxyglutamate (GLA) domain 1072-1113
R31237_1 h AAC3348	H	34	154	CAMK	EMK	729	UBA domain 327-365
406786.5 h	H	36	155	CAMK	EMK	1330	PAS domain 133-186, 247-280, 354-386
Z38720 h	H	41	181	CAMK	MLCK	874	WD domain, G-beta repeat 674-711
SGK088 h	H	42	182	CAMK	Trio	2287	Immunoglobulin domain 1-42, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-390, 1697-1779
R19772 h	H	44	184	CAMK	Trio	1287	RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain 419-528
1700013980197 h IRAH	H	76	195	Other	IRAK	598	Death domain 26-106
AA088547 h	H	78	197	Other	IRE	922	PQQ enzyme repeat 39-75
AA232253 h	H	82	201	Other	MLK	800	SAH domain (Sterile alpha motif) 337-408
AA599286 h	H	89	208	Other	SLOB	649	PX domain 18-122
AA836348 h	H	113	232	STE	NEK	836	Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650
PAK6 h	H	115	234	STE	STE20-02	719	P21-Rho-binding domain 11-69

FIGURE 1A

SEQ ID NO: 122_X69117_H BARK2_H
 MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN
 QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC
 SHPFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDI FQKFMESDKFTRFCQWKNV
 ELNIHMTMNEFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLDKKRIKMKQGETLALNER
 IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYATE
 IILGLEHVHNRVYRDLKPANILLDEHGHARISDLGLACDFS KKKPHASVGTGHYMAPE
 VLQKGTAYDSSADWFSLGCMFLKLLRGHSPFRQHKTCDKHEIDRMTLT VNVLPDTFSPE
 LKSLLEGLLQRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVVYLQKYPPLIPPRGEVNAA
 DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTETVYEAVNADTDKIEARK
 RAKNKQLGHEEDYALGKDCIMHGYMLKLGNPFLTQWQRRYFYLF PNRLEWRGEGESRQNL
 LTMEQILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKELNETFKEAQRLLRR
 APKFLNKPRSGTVELPKPSLCHRNSNGL

SEQ ID NO: 123_AA144574_M BARK2_M
 CFVVYRDLKPANILLDEYGHVRI SDLGLACDFS KKKPHASVGTGHYMAPEVLQKGT CYDS
 SADWFSLGCMFLKLLRGHSPFRQHKTCDKHEIDRMTLT VNVQLPDAFSPELRSLLLEGLLQ
 RDVSQRLGCGGGGARELKEHIFFKGIDWQHVVYLKYPPLIPPRGEVNAA DAFDIGSFDE
 EDTKGIKLLDCDQDLYKNFPLVISERWQQEVTETVYEAVNADTDKIEARKKAKNKQLGQE
 EDYAMGKDCIMHGYMLKLGNPFLTQWQRRYFYLF PNRLEWRGEGESRQSLTMEQIMSVE
 ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPR
 AILEFSKPPLCHRNSSGL

SEQ ID NO: 124_AA826850_H
 MGSSMSAATARRPVFDDKEDVNFDFHFI LRAIGKGSFGKVCIVQKRDT EKMYAMKYMNKQ
 QCIERDEVNRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ
 FSEDTVRLYICEMALALDYLRGQHI IHRDVKPDNILLDERGHAHLTDFNIATIIKDGERA
 TALAGTKPYMAPEIFXS FVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDIHSSNAVESLV
 QLFSTVSVQYVPTWSKEMVALLRKL LTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVE
 PGFVPNKGRLLHCDPTFELEEMILESRLHKKKKRLAKNKS RDNSRDSSQSENDYLQDCLD
 AIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125_AA960957_H
 MGGNHSKPPVFDENEEVNFDFHFI LRAIGKGSFGKVCIVQKRDT KMYAMKYMNKQKCI
 ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFT
 GTVKLYICELALALEYLQRYHI IHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM
 AGTKPYMAPEVFQVYMDRGP GYSYPVDWWSLGITAYELLRGWRPYEIH SVTPIDEILNMF
 KVERVHYSSTWCKGMVALLRKL LTKDPESRVSSLHDIQSVPYLADMNWDVAFKKALMPGF
 VPKGRLLNCDPTFELEEMILES KPLHKKKKRLAKNRSRDGT KDSCPLNGHLQHCLTVRE
 EFIIFNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNNLLTHTCTRGCS

SEQ ID NO: 126_TBK1_H
 MQSTSNHLWLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK
 KLNHNKIVKLFAIEEETTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV
 GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDEQFVSLYGT EYL
 HPDMYERAVLRKD HQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVMYKIITG
 KPSGAISGVQKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQFFA
 ETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHEL VYKQTKI ISSNQELIYEGRRLV
 LEPGRLAQHFPKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLGDASMAKAITG
 VVCYACRIASTLLLYQELMRKGIRWLI ELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE
GTHPKDRNVEKLQVLLNCMTEIYYQFKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHI LERFGSLTMD
GGLRNVDC L

SEQ ID NO: 127_AA305176_H
MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLQKGGKLYA
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGGDVKS
LLHIYGYFDEEMAVKYISEVALALDYLRHGGIIHRDLKPDNMLISNEGHIKLTDFGLSKV
TLNRDINMMDILTTPSMAPRQDYSRTPGQVLSLISSLGFNTPIAEKNQDPANILSACLS
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128_AA116841_M
TRPIWPPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV
PQPDDETDTSYFEARNNAQH LTVSGFSL

SEQ ID NO: 129_AA256100_H
MAMTAGTTTTFPM SNHTRERTVAKLTLENFY SNLILQHEERETRQKKLEVAMEEEGLAD
EEKLRRSQHARKETEFRLRLKRTRLGLDDFESLKVIGRGAFGEVRLVQKKDTGHIYAMKI
LRKSDMLEKEQVAHIRAERDILVEADGAWVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM
KKDTLTTEETQFYISETVLAIDAIHQ LGFIHRDIKPDNLLLDAGHVKLSDFGLCTGLKK
AHRTEFYRNLT HNPPSDFSQNMNSKRKAETWKKNRRQLAYSTVGTDPDIAPEVFMQTGY
NKLCDWWSLGVIMYEM LIGYPPFCSETPQETYRKVMNWKETLVFPPEVPISEKAKDLILR
FCIDSEN RIGNSGVEEIKGHPFFEGVDWEHIRERPAAIPIEIKSIDDTSNFD DFPESDIL
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQRGSIPTYMKAGKL

SEQ ID NO: 130_AA210825_H
DSL LPTPALGTPLPIPWVPGSLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG
SPLSHLLTRSRGSRTQGPPGPPGGSRVGSRRVAVPGLPPWPPPPHYAGLPGPSPGPGSP
PPGGLELQSPPLLPQIPAPGSGVSFHIQIGLTRE FVLLPAASELAHVQLACSIVDQKF
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVL SASATFEDFQIRPHAL
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLN YHKRCAFSIPNNCSGARKRRLSSTSL
ASGHSVRLGTSESLPCTAEELSRSSTELLPRRPPSSSSSSSASSYTGRPIELDKMLLSKV
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDCKFNCHKRCATRV PNDCLGEALIN
GDVPMEEATDFSEADKSALMDESEDSGVI PGSHSENALHASEEEEEGEGGKAQSS LGYIPL
MRVVQSVRHTTRKSSTTLREGWVVHYSNKD TLRKRHYWR LDKCITL FQNNTTNRYYKEI
PLSEILTVE SAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGT PGGPSGQGA EAARGLX
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEV LGS
QFGVVYGGKHKRTGRDVA VKVIDKLRFPTKQESQLRNEVAILQSLRHPGIVNLECMFETP
EKV FVMEK LHGDMLEMILSSEKGR LPERLT KFLITQILVALRHLHFKNI VHCDLK PENV
LLASADPF PQVKLCDFGFARI IGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVGVI
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAG AIDLINNLLQVKMRKRYSVDK
SLSHPW LQEYQTWLDLRELEGKMGERYITHESDDARWEQFAAEHPLPGSGLPTDRDLGGA
CPPQDHDMQGLAERISVL

SEQ ID NO: 131_AA127299_H
IQFIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKKTLTPTWNETFFVHFPEKTTLEL
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

FIGURE 1C

SEQ ID NO: 132_AA316804_H

MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV
SFLQLIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN
ILQLITSADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR
QGLKCEGCGLNYHKRCAPKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES
HVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSDSSRGLDDT
EESPSPEDKMFFLDPSDLDERDEEAVKTISPSTSNNIPLMRVVQSIKHTKRKSSTMVKE
GWMVHYTSRDNLKRHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG
SNPHCFEIIITDMVYFVGENNGDSSHNPLAATGVGLDVAQSWEKAIRQALMPVTPQASV
CTSPGQGDHDKDLSTSISVSNQCQIENVDISTVYQIFADEVLGSGQFGIVYGGKHKRKTGR
DVAIKVIDKMRFPKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVMEKHLHGDMLE
EMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEFPFQVKLCD
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSKGYNRSLDMWSVGVIIVVSLSGTFPFNEDE
DINDQIQNAAFMYPPNPWREISGEAIDLINLLQVKMRKRYSDKSLSHPLQDYQTWLD
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133_PKNBETA_H

MEEGAPRQPGPSQWPPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHGLGHVQQLLRSS
NRRLEQLHGELRELHARILLPGPGPGAEPVASGPRWAEQLRARHLEALRRQLHVELKV
KQGAENMTHTCASGTPKERKLLAAAQQMLRDSQLKVALLRMKISSLEASGSPEPGPELLA
EELQHRHLHVEAAVAEGAKNVVKKLLSSRRTQDRKALAEAQAQLQESSQKLDLLRLALEQLL
EQLPPAHLRSRVRELRAAVPGYPQPSGTPVKPTALTGTQLQVRLGCEQLLTAVPGRSP
AAALASSPSEGLWRLTKAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI
PLERARELEIGVHWRDWRQLCGVAFLRLEDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSSPSTISPPKGCPR
PTTLREASDPATPSNFLPKKTPLEEMTPPPKPPRLYLPQEPTSEETPRTKRPHMEPRTR
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLVQFKGTGKYAIKALKKQEVLSRDE
IESLYCEKRILEAVGCTGHPFLSLLVCFQTSSSHARFVTEFVPGDLMMQIHEDVFPEPQ
ARFYVACVVLGLQFLHEKKIYRDLKLDNLLLDQAQGLFKIADFGLCKEGIGFGDRTSTFC
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPG
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLC
GPADLRYFEGEFTGLPPALTPPAPHSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 134_AI021023_M_PKNBETA_M

LKWDNLLLDQAQGLFKIADFGLCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG
LGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA
GEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTPPAP
HSLLTARQQAARDFDFVSERFLEP

SEQ ID NO: 135_H19102_H

GGNIRGPWARGWKSLSWTGLGTIRSDLEELWELRGHHYHLHQESLKPAPVLVEKPLPEWPVP
QFINLFLPEFFPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVVLQR
DTVROCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYCSTDLYSLWSAVGCFPEASI
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFVAAERDHSVAMLASVTHSDSEIPAS
LNQGLSLLLHELLCQNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS
SAETMPFDDFDCDLESFLLYPIPA

FIGURE 1D

SEQ ID NO: 136_AA476563_H

MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFFTLPDGDSASRSFNTSESKVEFKAQ
 DTISRGSDDSVPVISFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN
 IGIENKLLLEAPDVLCLRLSTEQCQAHEEKGIEELSDPSGPKSYSITEKHQAQEDPRMLF
 VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTESLFRICSPLSGANEYIASTDT
 LKTEEVLLFTDQTDLLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS
 RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS
 CDSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP
 ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPPFTPDWAELMR

SEQ ID NO: 137_AA626690_H

MLPFAPQDEPDREMEVFSGGGASSGEVNGLMVDEPMEEGEADSCHDEGVVKEIPITHH
 VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT
 KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTTEEDVKFYLA
 ELALALDHLHQLGIVYRDLKPENILLDEIGHIKLTDFGLSKESVDQEKKAYSFCGTVEYM
 APEVNNRRGHSQSADWWSYGVLMFEMLTGTLPFQKGKDRNETMNMILKAKLGMPQFLSAEA
 QSLRLMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDFTFCF
 DPEFTAKTPKDSPLPASANAHQLFKGFSFVATSIAEYKITPITSANVLPVQINGNAA
 QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI
 ITLKDVFDGRYVYLVTDLMKGGELLDRILKQKCFSEASDILYVISKTVDYLHCQGVV
 HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGLLLTPCYTANFVAPEVLMQQGYD
 AACDIWSLGLVLYFTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL
 SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ
 PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138_AA215680_H

MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPDMTKRDYLVDAATQIRLA
 LERDVSEDEYEAFFNHQNGVDVLLRGIHVDPNKRREAVKLKITKYLRRAEEIFNCHLQR
 PLSSGASPSAGFSSLRLRPIRTLSSAVEQLRGCRVVGVIKQVLVQDPATGGTFVVKSLP
 RCHMVSRLRTIIPHGVPYMTKLRLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL
 SSGSTQERMKAQLNPHLNLTPARLPSGHAPGQDRIALEPPRTSPNLLLAGEAPSTRPQR
 EAEGEPTARTSTSGSSDLPKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG
 RGMDSCLSDAGARGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL
 DQAGHIRLTYFGQWSEVEPQCCGEAVDNLVSAPEVGGISELTEACDWWFSGSLLYELLTG
 MALSQSHPSGIAHTQLQLPEWLSRPAASLLTELLQFEPTRRRLGMGEGGVSKLKSHPFFS
 TIQWSKLVG

SEQ ID NO: 139_SGK_H

MTVKTEAAKGTLYSRMRGMVAILIAFMKQRRMGLNDFIQKIANNYACKHPEVQSILKI
 SQPQPELMNANPSPPPSPSQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKAE
 EVFYAVKVLQKKAILKKKEEKHIMSENVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
 GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
 FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSR
 NTAEMYDNILNKPLQLKPNITNSARHLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW
 DDLINKKITPPFNPVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG
 FSYAPPTDSFL

SEQ ID NO: 140_AA107515_M

MTVKAEAAARSTLYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM
 SHPQPELMNANPSPPPSPSQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKAE

FIGURE 1E

EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
XFQLRRRIEHN GTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN
TAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD
DLINKKITPPFNPVNSGSPDLRHFDPFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF
SYAPPVDSFL

SEQ ID NO: 141_AA109508_M

HLQRRERFLEPRARFYAAEVASAI GYLHSLNIIYRDLKPENILLDCQGHVVLTDFGLCKE
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVSQMY
ENILHQPLQIPGGRTVAACDLLQSLHDKDQRLGSKADFLEIKNHVFFSPINWDDLYHK
RLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD
ILDC

SEQ ID NO: 142_AA887783_H

MQRDHTMDYKESCPVXIPSSDEHREKKKRFTVYKVLVSVGRSEWVFVRRYAEFDKLYNT
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMD
SPKHQSDPSEDEDERSSQKLHSTSONINLGPSGNPHAKPTDFDFLKVIGKGSFGKVLLAK
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKHPFLVGLHYSFQTTEKLYFVL
DFVNGGEGHVLTDFGLCKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTVDWWCLGAV
LYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSI LEELEKDRQNLGAKEDF
LEIQNHPPFESLSWADLVQKKIPPPFNPVAGPDDIRNFDTAFTEETVPYSVCVSSDYSI
VNASVLEADDAFVGFSYAPPSDFL

SEQ ID NO: 143_R47805_H

MAHQGTGIHATEELKEFFAKARAGSVRLIKVVIEDEQLVLGASQEPVGRWDQDYDRAVLPL
LDAQQPCYLLYRLDSQNAQGFEWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDE
LFGTVKDDLSFAGYQKHLSSCAAPLTS AERELQQIRINEVKTEISVESKHQTLQGLAF
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL
YKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIAKKIEIGDG
AELTAEFVLYDEVHPKQHAFAKQAFAPKPGPGGKRGRHLIRGPGENGDDS

SEQ ID NO: 144_H60215_H

MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR
KDGTDDFYQLKILTLEERGQDQIESQEERQGM L LHT EYSLLSLLHTQDGVVHHHGLFQD
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV
VIFYDVVRVVEALHQKNIVHRDLKLGNMVNLNRTHRITITNFC LGKHLVSEGDLKDQRG
SPAYISPDVLSGRPYRGKPSDMWALGVVLTMLY GQFPFYDSIPQELFRKIKAAEYTIPE
DGRVSENTVCLIRKLLVLDPQORLAAADVLEALS AIIASWQSLSSLSGPLQVVPDIDDQM
SNADSSQEAKVTEEC SQYEFENYMRQQLLLAEKSSIHDTRSWVPKRQFGSAPPVRLGH
DAQPMTSLDTAILAQRYLK

SEQ ID NO: 145_SGK324_H

MASTRSIELEHFEERDKRPRGSRGAPSSSGSSSGPKGNGLIPSPAHSAHCSFYRTR
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGTSRALAAA
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLT DITEAIKXASG
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVL DHSECRVLKSSYS
RSSAVKYSGSKSPGSRRSQISAHGRSSSNVNGPELDRCSPEGVNGNRCSESSTLLEK
YKIGKVIGDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH
RDIKPENLLVCEYPDGTSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD
IWAAGVITYIILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ
VNVEARCTAGQILSHPWVSDDASQENNMQA EVTGKLGKQHFNNALPKQNSTTTGVSVMVS
GRRQVWPCGAGLEVFE LGSRELPSHGSWCLP

SEQ ID NO: 146_W30246_M SGK324_M

TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSP EGVNGNRCSESFP LLEKYR
IGKVIDGDNFAVVKECDRYTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNIIML
VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHSLSIVHRD
IKPENLLVCEYPDGTSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW
AAGVITYIILLCGFPPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147_AA383293_H

PAAKRVVYRNGDPFFPGSQLVVTQRRFPTMEAF LCEVTS AVQAPLAVRALYTPCHGHPV
TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPFSLKLSQAASQDWETVL
KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDL PYPALSTRGLLAA
GNEAHLRSGVGT VAGSPKPLGRKAKKETCLIVTLTLKYQQSETSRDGQSFP SGVIGVYGA
PHRRKETAGALEVADDED TQTEEPDQRAAQIVEQVTC LQDFFGDDDVFIACGPEKFRYA
QDDFVL DHSRRRLREHQAGFEKLRRTRGEEKEAEKEKPCMSGGRMTLRDDQPAKLEK
EPKTRPEENKPERPSGRKPRPMGIIAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYA
MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLI L EYVQGGDLFDAI
IESVKFPEPDAA LMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEDKSTTLKLADFGLA
KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYIILLCGFPPFRSPXXGDQDE
LFNIIQLGHFEFLPPYWDNISDAAKDLVSRLLVDPKKRYTAHQVLQHPWIETAGKTNTV
KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148_AA197883_M

MPTAPVLRPPPPATPAPPAPSRPAPP I P GHRGPCDHS LKCLSSKISERKLPGPWL PAGR
GPLEKPVLGPRGAVMPLFSPQSSLSHVRAHSPLKPRVVT VVKLGGQPLRKATLLLNRRS
VQTFEQLLSDI SEALGFPRWKNDVRKLF T LKGREVKSVSDFFREGDAFIAMGKEPLTLK
SIQLAMEELYPKNRALALAPHSRVPSRLRSRLPSKLLKGSHRCGEAGSYSAEMESKAVS
RHQGKTSTVLAPEDKARAQKWVRGKQSESEPGGPPSPGAATQEETHASGEKHLGVEIEKTS
GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRPSKAKFTD
GEEGWKGDSHRGSPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQGA PKAQKDFVEGPPAV
EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPLPRTRGEEKQAEHEKKPGGLGERRAPE
KESKRKLEEKRPERPSGRKPRPKGII SADVEKHYDIGGVIGDGNFATVKECRHRETKQAY
AMKMIDKSQ LKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA
IVENVKFPEPEAAVMITDLCKAFVHMHDKNIVHRDVKPENLLVQRNEDKSITLKLADFG L
AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYIILLCGFPPFRSPERDQDE
LFNIIQVGQFEFLSPYWDNISDAAKDLVRNLLVDPKKRYTAEQVLQHPWIEMVGHTNTG
NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149_DRAK2_H

MSRRRFDCRSISGLLTTPQIPIKMENFNNFYILTSKELGRGKFAVVRQCISKSTGQEYA
AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS
LCLPELAEMVSENDVIRLIKQILEGVYYLHQNNIVHLDLKPQNILLSSIYPLGDIKIVDF
GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYNLISQVNVNDYSEETFSSVSQ L ATDFIQSLLVKNPEKRPTAEICLSHSLWQQWDFEN

FIGURE 1G

LFHPEETSSSSQTQDHSVRSSSEDKTSKSSCNGTCGDREDKENI PEDSSMVSKRFRFDDSL
PNPHELVSDDLCC

SEQ ID NO: 150_W44160_M DRAK2_M
MSRRRFDCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA
AKSLKKRRRGQDCRAEILHEIAVLELARSCPHVINLHEVYENATEIILVLEYAAGGEIFN
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNNIVHLDLKPQNILLSSIIYPLGDIKIVDF
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYNISQVNVYSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENI PEDGSLVSKRFRFDDSL
PSPHELVPDLFC

SEQ ID NO: 151_H01248_H, DRAK1_H
MIPLEKPGSGGSSPGATSGSGRAGRLSGPCRPPPPQARGLLTEIRAVVRTEPFQDGYS
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEIIEHIAVLELAQDNPW
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR
DVVHLDLKPQNILLTSESPLGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI
SMATDMWSIGVLTIVMLTGISPLGNDKQETFLNISQMNLSYSEEEFDVLSESAVIDFIRT
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDTDKSE
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAISKRFKFEEPLLQEIPGEFIY

SEQ ID NO: 152_AA021445_H
MPARIGYYEIDRTIGKGNFAVVKRATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF
CHCRNIVHRDLKAENLLLDANLNIAIDFGFSNLFPTGQLLKTWCGSPPYAAPELFEGKE
YDGPVKDIWSLGVVLYVLVCGALPFDGSTLQNLRLARVLSGKFRI PPFMSTECEHLIRHML
VLDPNKRLSMEQICKHKWMKLGADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL
DKEQTLQSLRSDAYDHYSAIYSLCDRHKRHKTLRLGALPSMPRALAFQAPVNIQAEQAG
TAMNISVPQVQLINPENQIVEPDGTLNLDSDGESEPSPEALVRYLSMRRTVGVADPRT
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNLPMQNLOPTGQLEYKEQSLLQPPTLQ
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPO
EAVQRYLANRSKRHTLAMTNPTAEIPPDQRQLGQQPFRSRVWPPHLVPDQHRSTYKDSN
TLHLPTERFSPVRRFSDGAASIQAFAHLEKMGNNSSIKQLQCECEQLQKMYGGQIDERT
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQPSPLQAACENQPALLTHQLRLRIQPS
SPPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQPENCSSPPN
VALTCLGMQQAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMOMQHRTNL
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYPDQAHLPPLFSDQSRGSPSSYSPST
GVGFSPTQALKVPPLDQFPTFPPSAHQPPHYTTSALQQALLSPTPPDYTRHQQVPHILO
GLLSPRHSLTGHSIDIRLPPTFAQLIKRQQQQRQQQQQQQQQEQEYQELFRHMNQGDAGSL
APSLGGQSMTERQALSQYQADSYHHHTSPQHLLQIRAQECVSQASSPTPPHGYAHQPALM
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG
IHPYGHQPTAAFSKNKVPSREPVI GNCMDRSSPGQAVELPDHNGLGYPARPSVHEHHRPR
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE
CGASLGGHEHPDLSDGSQHLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153_2R22-5-11_H
MTAVYMNGGGLVNPYARWDRRDSVESGCQTESSKEGEEGQPRQLTPFEKLTQDMSQDEK
VVREITLGKRIGFYRIRGEIGSGNFSQVKLGIHSLTKEKVAIKILDKTCLDQKTQRLLSR
EISSMEKLHHPNIIIRLYEVVETLSKLHLVMEYAGGGELFGKISTEGKLSEPESKLIFSQI
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

FIGURE 1H

LFRDEHYIGIYVDI WALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR
LIRGVLQQIPTERYGIDCIMNDEWMQGVPTPLEPFQLDPKHLSETSTLKEEENEVKST
LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPVMMLPDPKERDLKKGS
RVYRGIRHTSKFCSIL

SEQ ID NO: 154_R31237_1_H, AAC33487

MSTRTPLTVNERTENHTSHGDGRQEVTSRTSRSGARCRNSIASCADQPHIGNYRLLK
TIGKGNFAKVKLARHILTGREVAIKI IDKTQLNPTSLQKLFREVRIMKILNHPNIVKLFE
VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK
AENLLLDADMNIKIADFGFSNEFTVGGKLDTCGSPPYAAPELFQGGKYDGPEDVWSLG
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRGTLQ
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT
YLLLGRKSSSELDASDSSSSSLAKVRPSSDLNNSTGQSPHHKVQSVSSSQKQRRYSD
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPMLGNASPNK
ADI PERKKSSTVPSSNTASGGMTRRNTYVCSERTTADRHSVIQNGKENSTIPDQRTPVAS
THSISSAATPDRI RFPRGTASRSTFHGQPRERRTATYNGPPASPSLSHEATPLSQTRSRG
STNLF SKLTSKLTRSRNVAEQDENKEAKPRSLRFTWSMKTSSMDPGDMMREIRKVL D
ANNCDYEQRRERLLFCVHGDGHAENLVQWEMEVCKLPRLSLNGVRFKRISGTSIAFNIA
SKIANELKL

SEQ ID NO: 155_W90839_M

KGPSWSSRSLGARCRNSIASCPEEQPHVGNRYLLRTIGKGNFAKVKLARHILTGREVAIK
I IDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIETEKTLYLMYASAGEVFDYLV
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLDAAENIKIADFGFSNEFTL
GSKLDTCGSPPYAAPELFQGGKYDGPEDVWSLG VILYTLVSGSLPFDGHNKELRERV
LRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE
RMPGRKASCSAVGSGSRGLPPSSPMVSSAHNPNAEIPERRKDSTSTPNNLPPSMMTRRN
TYVCTERPGSERPSLLPNGKENSSGTSRVPPASPSHSLAPPSGERSRLARGSTIRSTFH
GGQVRDRRAGSGSGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLTSKLTRRVTD E
PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156_406786.5_H

MEVGGLTVFEEDQRCLSQSLPLPVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSRLCQS
RTALSEDRWSSYCLSSLAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS
PLLAPVCNPNKAIFTVDAKTTEILVANDKACGLLYSSQDLIGQKLTQFFLRSDSDVVE
ALSEEHMEADGHA AVVFGTVVDIITRSGEKIPVSVWMKRMQRERRLCCVVVLEPVERVST
WVAFQSDGTITSCDSLFAHLHGYSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIQRSV
GRARDGTTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI
NHSFALTFLGYGKTELLGKNITFLIPGFYSYMDLAYNSSQLPDLASCLDVGNESGGER
TLDPWQGDPAEGGQDPRINVVLAGGHVVPREIRKLMEQDIFTGTQTELIAGGQLLSC
LSPQAPAGVDNVPEGSLPVHGEQALPKDQQTALGREEPVAIESPGQDLLGESRSEPVDV
KPFASCEDSEAPVPAEDGSDAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ
LAGGSLLMHCPYGEWGLWWSQDLAPSPSGMAGLSFGTPTLDEPWLGVEN DREELQTC
LIKEQLSQLSLAGALDVPHAELVPTCEQAVTAPVSSCDLGGRDL CGGCTGSSSACYALAT
DLPGGLEAVEAQEVDVNSFSWNKELFFSDQTDQTSNCS CATSELRETPSSSLAVGSDPD
VGS LQE QGSCVLDRELLLTGTCTVDLGQGRRFRESCVGHDPTEPLEVCLVSSEHYAASD
RESPGHVPSTLDAGPEDTCPSAEPRLNQVQVSTPVI VMRGAAGLQREIQEGAYSGSCYH
RDGLRLSIQFEVRRVELQGPTPLFCCWLVKDLLHSQRDSAARTLFLASLPGSTHSTAAE
LTGPSLVEVLRARPWFEEPPKAVELEGLAACEGEYSQKYSTMSPLGSGAFGFVWTAVDKG
KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLEIAILSRVEHANI KVL DIFENQGGFFQLV

FIGURE 11

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDI IHRDIKDEN
 IVIAEDFTIKLIDFGSAAYLERGKLFYTFCTIEYCAPEVLMGNPYRGPELEMWSLGVTL
 YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQVPERRTTLEKLVTDWPVWTO
 PVNLADYTWEVFRVKNKPESGVLSAASLEMGNRSLSDVAQAQELCGGPVPGAPNGQGCL
 HPGDPRLLTS

SEQ ID NO: 157_AA544838_M 406786_M
 TRPHPCLDPLASFIHQVLSAVGYLHSGQI IHRDIKDENIVIAEDFTIKLIDFGSAAYL
 ERGKLFYTFCTIEYCAPEVLIGNPYRGPELEMWSLGVTLTYTLIFEENPFCEVEETMEAV
 IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLI RDPWVTQPVNLASYTWEVCRTNQPS
 GLLSAASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPSPVPS

SEQ ID NO: 158_AA785735_H
 MVMADGPRHLQRGVVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKI IDKSQLDVN
 LEKIYREVQIMKMLDHPHIIKLYQVMETKSMYLVTEYAKNGEIFDYLANHGRLNESEAR
 RKFWQILSAVDYCHGRKIVHRDLKAENLLLDNNMNIKIADFGFGNFFKSGELLATWCGSP
 PYAAPEVFEGQQYEGPQLDIWSMGVVLVYVLCGALPFDGPTLPILRQRVLEGRFRIPIYFM
 SEDCEHLIRRMVLDPKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV
 LRLMHSGLIDQQKXIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
 AEQTVAKAQTVGLPVTMHSNMRLLRSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT
 PKVNGCLDPVPPVLRKGCQSLPSNMETSIDEGLETEGEAEEDPAHAFAEFQSTRSGQ
 RRHTLSEVTNQLVVMGAGKIFSMNDSPSLDSVDSEYDMGSVQRDNLNFDENPSLKDIML
 ANQPSRMTSPFISLRPTNPAMQALSSQKREVNHRSPVSFREGRRASDTSLTQGIVAFRQ
 HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
 LPASVHPQSLPRQSLETQYLQHLQKPSLLSKAQNTCQLYCKEPPRSLEQQQLQEHRLQOK
 RLFLQKQSLQAYFNQMQUIAESSYPQPSQQLPLPRQETPPPSQQAPPFSLTQPLSPVLEP
 SSEQMYSFPLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPA
 PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDLTGPDPCPRSPGLQEAPSSYDPLAL
 SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159_AA207220_H
 MESLVFARRSGPTPSAAELARPLAELIKSPKPLMKKQAVKRHHKHNLRHRYEFLETGLG
 KGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIEHVEFE
 NSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVVRDLKLEN
 ILLDANGNIKIADFGLSNLYHQGKFLQTFCSPLYASPEIVNGKPYTGPEVDSWSLGVLL
 YILVHGTMFPDGDHDKILVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS
 HWWVNWGYATRVGEQEAPHEGGHGPSDSARASMAWLRSSRPLENGAKVCSFFKQHAP
 GGGSTTPGLERQHSLLKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPGKILKKKVSASA
 EGVEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYYSPEPSESSELDDAGDVV
 SGPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGLDELAPRPLARASRP
 SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGGSGCLRRWRQDP
 LGDSCFSLTDCQEVTTATYRQALRVCSKLT

SEQ ID NO: 160_AA426580_H, MAK_V_H
 MPAAAGDGLGEPAPGGGGGAEDAAAPAAACEGSFLPAWVSGVPRERLRDFQHHKRVGN
 YLIGSRKLGEGSFAKVREGLHVLTKGEKVAIKVIDKKRAKDTYVTKNLRREGQIQMIRH
 PNITQLLDILETENSYYLVMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA
 GVVRDLKNIENLLDEDNNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY
 GPKIDVWSIGVNMAMLTGTLPTVEPFSRLALYQKMDKMNPLPTQLSTGAISFLRSL
 LEPPDPVKRPNIQQALANRWLNENYTGKVP CNVTYPNRI SLEDLSPSVVLHMTKLGKYN

FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLQCYKTRLYQIEKYRAPKESYEA
SLDTWTRDLEFHAVQDKKPKEQEKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA
LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNCVASSSMEFIPVPPPRTPRIVKKPEPHQP
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS
PGLPSGMSPLHTPLHPTLVSFHEDKNSPPKEEGLCCPPPVPSNGPMQPLGSPNCVKSR
GRFPMMGIGQMLRKRHQSLSQPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161_Z36720_H

MDTKLNMLNEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI
DTQAGWPEVLELVAMQQDAAQHGARLEALFRMVAVDRAIALVGATFQKSKVADFLMQG
RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQDKGELSAEQGIWATLMTLV
IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIRASGLG
ADPAQAVVSPGQGDGVPQPAQAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAPGRVNV
VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTPGPGPQCPGPPGLPAQARATHSGGETPP
RAALLKGAVAPGFSRRDLVFPSIFCACLGISIHIEQMDTPGEMLMTGRGSLGPTLTTEAP
AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEEQRAGAEPG
TRPSLARSDDNDHEVGALGLQQKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEAGSV
VLDDSPAPPAPFEHRVVSVKETSISAGYEVQCHEVLGGGRFGQVHRCTEKSTGLPLAAKI
IKVKSADREDVKNEINIMNQLSHVNLILQLYDAFESKHSCTLVMEYVDGGELFDRITDEK
YHLTELDVVLFTTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKI IDFGGLARRYKP
REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLLSGLSPFLGETDAETMNFIV
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNNLPAKASRSKTRLK
SQLLLQKYIAQRKWKKHFYVVTAAANRLRKFPPTSP

SEQ ID NO: 162_SGK088_H

GEMALFECLVAGPTDVEVDWLRCGRLLQPALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC
KLSTAKDELTCARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVTWTHFG
CPMEESENLRLRQDGGHLHSLHIAHVGESEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAAS
GPSSKLEKMPISIPPEPEQGELERLSIPDFLRPLQDLEVGLAKEAMLECQVTGLPYPTISW
FHNHRIQSSDDRRMTQYRDVHRLVFPVAVGPQHAGVYKSVIANKLGAACYAHLYVTDVV
PGPPDGAPQVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQHQLVGLSDQWTALVTGLRE
PGWAATGLRKGVQHI FRVLSTTVKSSSKPSPSEPVLLEHGPTLEEAPAMLDPDIDVYV
VEGQPASVTVTFNHVEAQVWVRSCRGALLEARAGVYELS QPDDDQYCLRI CRVSRRDMGA
LTCTARNRHGTQTC SVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD
EVLLTESSHVSFVYEENECSLVVLSTGAQDGGVYTCTAQNLAGEVSCKAELAVHSAQTAM
EVEGVGEDEHRRRLSDFYDIHQEI GRGAFSYLRRIVERSSGLEFAAKFI PSQAKPKAS
ARREARLLARLQHD CVLYFHEAFERRRGLVIVTELCTEELLER IARKPTVCESEIRAYMR
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRI CDFGNAQELTPGEPQYCQYGT
EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFVGENDRTTLMNIRNYNVAFEETTF
LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKFLSRRRWQRSQ
ISYKCHLVLRPI PELLRAPPERVWVTMPRRPPSGGLSSSSDSEEELEELPSVPRPLQP
EFGSGSRVSLTDI PTEDEALGTPETGAATPMDWQEQGRAPSQDQEAPSPEALPSPGQEPAA
GASPRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG
EYAQRLQALRQRLLRGGPEDGKVSGLRGPLLES LGGRARDPRMARAASSEAPHHQPPLE
NRGLQKSSSFSGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQSSPARP
SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVRASKPAPPQALQTLALP
LTPYAQIIQSLQLSGHAQGPSQGPAAPPSEPKPHA AVFARVASPPPGAPEKRVPSAGGPP
VLAEKARVPTVPPRPGSSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG
PFRGAEEEDGIYRPS PACTPLELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRT
PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQRSGSSSEDSSGGAS

FIGURE 1K

GRSTPLFGRLRRATSEGESLRRLLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES
 RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPVFHIIKLDQVLLEGEAA
 TLLCLPAACPAPHISWMKDKKSLRSEPSVIIVSCKDGRQLLSIPRAGKRHAGLYECSATN
 VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW
 HPVSSGIPDCYYNVTHLPVGVTVRFRVACANRAGQGPFSSNSSEKVFVRGTQDSSAVPSAA
 HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSLKAVGPP
 PQTPRRHRGLQAARPAEPTLPSTHVTPEPKPFVLDGTPIIPASTPQGVKPVSSSTPVY
 VVTSFVSAPPAPPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP
 PQKPYTFLEEKARGRFGVVRACRENATGRTFVAKIVPYAAEGKPRVLQYEVLRTLHHER
 IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFYSEDDVATYMVQLLQGLDYLHGHHV
 LHLDIKPDNLLLAPDNALKIVDFGSAQYPNPQALRPLGHRTGTLEFMAPEMVKGEPISGA
 TDIWGAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFADFQLYPNTS QSATLFLRKVLSV
 HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRRAEAATRHKVLLR
 SYPGGP

SEQ ID NO: 163_AA542015_M SGK088_M

ATDIWGAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFADFQLYPNTS QSATLFLRKVLS
 VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRRAEAATRHKVLL
 RSYPGSP

SEQ ID NO: 164_R19772_H

MKGGDRAYTRGPSLGWLFACCCCFPCRDAYSHSSSENGGKSESVANLQAQPSLNFIIHSS
 PGPKRSTNTLKKWLTSPVRRNLNSGKADGNIKKQKKVRDGRKSF DLGSPKPGDETTPQGDS
 ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLLAARQASTEVPTAADLVNA
 IEKLVKNKLSLEGSSYRGLKDPAGCLNEGMAPPTPPKNPEEEQKAKALRGRMFVLNELV
 QTEKDYVKDLGIVVEGFMKRIEEKGVPEMDRGKDKIVFGNIHQIYDWHKDFFLAELEKCI
 QEQDRLAQLFIKHERKLHIYVWYCNKPRSEYIVAEYDAYFEEVKQEIINQRLTSLDFLIK
 PIQRITKYQLLLKDFLRYSEKAGLECS DIEKAVELMCLVPKRCNDMMNLGR LQGFEGTLT
 AOGKLLQQDTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGS LTPGYMFKRSIKMN
 YLVLEENVNDNDPCKFALMNRETSE RVVLQANADIQQAWVQDINQVLETQRDFLNALQSP
 IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPPLKISTSNQSP
 GFHEYHQPGDKFEASKNDLGGCNGTSSMAVIKDYYALKENEICVSQGEVVQVLAVNQQNM
 LUYQPASDHSPAAGWVPGSILAPLT KATAAESDGSIKKSCSWHTLRMRKRAEVENTGK
 NEATGPRKPKDILGNKVS VKETNSSESECDLDPNTSMEILNPNFIQEVAPFLVPLVD
 VTCLLGDTVILQCKVCGRPKPTITWKGPQDNI LDTDNSSATYTVSSCDSGEITLKI CNLM
 PQDSGIYTCIATNDHGTTSATVKVQGVPAAPNRPIAQERSCTSVILRWLPPSSTGNCT
 ISGYTVEYREEGSQIWQQSVASTLD TYLVIEDLSPGCPYQFRVSASN PWGISLPSESEF
 VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATRKDVAVK FVNKKM
 KKKEQA AHEAALLQHLQHPQYITLHD TYESPTS YILILELMDDGRLLDYL MNHDELMEEK
 VAFYIRDIMEALQYLHNC RVAHLDIK PENLLIDLRI PVPRVKLIDLEDAVQISGHFHIHH
 LLGNPEFAAPEVIQGI PVSLGTDIWSIGVLT YVMLSGVSPFLDESKEETCINVC RVDFSF
 PHEYFCGVSN AARDFINVLQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI
 ERRKHQNDVRPIPNVKS YIVNRVNQGT

SEQ ID NO: 165_5R72_8_2_H

MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLV VEMSQTSSIGSAESLISLERK
 KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEEIIYTFGR
 ILGKGSFGIVIEATDKETETKWA IKKVNKEKAGSSAVKLLEREVNILKSVKHEHIHLEQ
 VFETPKKMYLMELCEDGELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHRDLK
 LENIMVKSS LIDDNNEINLNIKVTD FGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPPFLASSEAKLFELIRKGE LHFENAVWNSISDCAKSVLKQ
LMKVDPAHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEENKPS
TEEKLKSYQPWGNVPETNYTSDEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE
IKGEMEKTPVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166_SGK309_H

MQCLAAALKDETNMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN
ALKVESAAQQPKQVLKMEVAVLKKLQSGSLGQGDGKEEMMKPGAKRGKDHVCRFIGCGRNE
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESEIAIHSVGLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHD
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMKEKEYEHRMLLKHMPSEFHLFLDHIASLDY
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG
GQCDASAWGPAPGEHRGCATGRAPEXPGECTPNSAREALXGAGPQSPPCPPPRGSXGXSL
GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLLSPPIPSLVPLPCSSXAPCPPPIISLLARPLF
PVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167_AA234451_H

MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAAQQPKQV
LKMEVAVLKKLQGDHVCRFICGRNDRFNVVMQLQGRNLADLRRSQSRGTFTISTTLR
LGRQILESIESIHSVGSXHRDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP
RAVAGFRGTVRYASINAHNRNEMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE
RYDHRLMLKHLPPFSIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT
GNDGSLTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP
VGVSPDKLPGSLGHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL
GSPIRVRSEITQPDRIPLVRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168_AA435956_H

TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSFQLFMFQLLRGLAYIHHQHVLHRDLKPQN
LLISHLGELKLADFLARAKSIPSQTYSSSEVTLWYRPPDALLGATEYSSELDIWGAGCI
FIEMFQGQPLPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPWFPLPTPRSLHV
VWNRLGRVPEADLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV
RLKPEMCDLLASYQKGHPAQFSKCW

SEQ ID NO: 169_AA626859_H

NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIKICDFGFAQILIPGD
AYTDYVATRWRAPPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
TLGKLI PRHQSI FKSNGFFHGISIPEPEDMETLEEKFSVDVHPVALNFMKGCLKMNPDRL
TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQNQLLPLIPGSHISPTPDGRKQVLQLK
FDHLPNI

SEQ ID NO: 170_AA061797_M

KIALREIRMLKLKHPNLVNLIIEVFRKRKMHVFEYCDHTLLNELERNPNGVSDGVIKSV
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMIKICDFGFARILIPGDAYTDYVATRWY
RAPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI PRHQSI
IFRSNQFFRGISIPEDMETLEEKFSNVQPVALSFMKGCLKMNPDRLTCAQLLDSAYF
ESFQEDQMKRKARSEGRSRRRQQNQLLPLIPGSHISPTPDGRKQVVQLKFDHLPNI

SEQ ID NO: 171_AA397553_H

MPNSERHGGKKDGGSGASGTLQPSGGGSSNSRERHRLVSKHKRHSKHSKMDGLVTPEA
ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSDRLHKHRHHQHRRSR

FIGURE 1M

DLKAKQTEKEKSQEVSSKSGSMKDRISGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH
KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSOSSKQDDSPSGA
SYGQDYDLSPSRSTSSNYDSYKSPGSTSRRQSVSPPYKEPSAYQSSTRSPSPYSRRQR
SVSPYSRRRSSSYERSGSYSGRSPSPYGRRRSSSPFLSKRSLRSPLPSRKSMKSRSRSP
AYSRHSSSHSKKRSSSRSRHSSI SPVRLPLNSSLGAELSRKKKERAAAAAAKMDGKES
KGSPVFLPRKENS SVEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTVKNSSDTGK
VKLDENSEKHLVKDLKAQGTDRSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPPLP
TTTTPPPQTPPLPLPPIPALPQQPPLPPSPAFSQVPASSTSTLPPSTHSKTS AVSSQAN
SQPPVQVSVKTVQSVTAAPHLKTSTLPPPLPLPPLPGGDDMDSPKETLPSKPVKKEKEQ
RTRHLLTDLPLPELPGGDLSPDSEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG
KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPITAIREIKILRQ
LIHRSVNMKEIVTDKQDALDFKDKGAFYLVFEYMDHDLMLLESGLVHFSEDHIKFSM
KQLMEGLEYCHKKNFLHRDIKCSNILLNNSGQIKLADFLARLYNSEESRPYTNKVITLW
YRPPPELLLGEERYTPAIDVWSCGICLGELFTKKPIFQANLELAQLELISRLCGSPCPAVW
PDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLLDHMLTLDPSKRCTAEQTLQSDFL
KDVELSKMAPDPLPHWQDCHELWSKKRRRQSQSGVVVEEPPPSKTSRKETTSGTSTEPVK
NSSPAPPQPAPGVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDL SIPQMAQLLNI
HSNPEMQQLEALNQSISALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS
STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQGPRRTPTMPQEEAAACPPHIL
PPEKRPPEPPGPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPEH
QALRPMEYSTRPRPNRTYGNTDGPETGFS AIDTDERN SGPALTESLVQTLVKNRTFSGSL
SHLGESSSYQGTGSVQFPDQDLRFARVPLALHPVVGQPFLKAEGSSNSVVAETKLQNY
GELGPGTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGPY

SEQ ID NO: 172_AA789239_H

MEMYETLGKVGESYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE
NLVNLIEVFRQKKKIHLVFEFIDHTVLDLQHYCHGLESKRLRKYLFQILRAIDYLHSNN
VIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVLDKTSYG
KYVPVDI WALGCMIIEMATGNPYLPSSSDLDLLHKIVLKVXFMPELKAKLLQEAQVNSLI
KPKESSKENELRKDERKT VYTNTLLSSSVLGKEIEKEKKPKEIKVRVIKVKGGRGDI SEP
KKKEYEGGLGQDANENVHPMSPTKLV TIEPPNPINPSTNCNGLKENPHCGGSVTMPPI
NLTNSNLMAANLSSNLFHPSVRLTERAKKRRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI
FNERTGHSDQMANENKRKLNFPSRDRKEFHFPPELPVTIQSKDTKGMEVKQIKMLKRESKK
TESSKIPTLLNVDQNEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173_AA124976_M

LADIVHACLQIDPAERTSSTDLLRHDFYTRDGFIEKFIPELRAKLLQEAQVNSFIKPEN
FKENEPVRDEKKS VFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIKAKGGKGDVPDQKKP
EYEGDHRQQTADDTQPSSLDKKPSVLELTNPLNPSSENSDGVKEDPHAGGCMIMPPINLT
SSNLLAANLSSNLSHPNSRLTERTKKRRTSSQTIGQTLSNSRQEDTGPTQVQTEKGAFNE
RTGQNDQISSGNKRKLNF PKCDRKEFHFPPELPFTVQAKEMKGMEVKQIKVLKRESKKTDS
SKIPTLLSMDPNQEKQEGGDGDCGKLNLRNRRFFFSR

SEQ ID NO: 174_AA575635_M CCRK_M

SASGQLKIADFLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVDLWAVGCIMG
ELLNGSPLFP GENDIEQLCCVLRILGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVL P
DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTAPLPAHPSELPIPQRPGGPAPKAHP
GPPHVDFHVDPRPIEESLLNPELIRPFIPEG

FIGURE 1N

SEQ ID NO: 175_AA631990_H

MITISISTEKGSHTHYPFMITTLQYYRGRGGKTAVWRHFS AEGPFAFAEMRH SKRTHCPDW
DSRESWGHE SYRGSHKRKRSHSSTQENRHCKPHHQFKESDCHYLEARSLNERDYRDRRY
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNRHCSSHQSR SXEIV
DTLGE GAFGKVVECIDHGMDGMHVAVKIVKNVGRYREARSEIQVLEHLNSTDPNSVFR C
VQMLEWFDHGHGVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHNNKL
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKN TDIKVVD FGSATYDDEHHS TLVSTRH
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGP I PQHMIQ
KTRKRKYFHNNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLF DLVRRMLEYDPTQ
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176_AA557536_H

MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA
PEHSPSWPSSRLRLSPQEFGDHPNII SLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGG L
LQDVHVRSIFYQLLRATRFLHSGHVVRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG
PEDQAVTEYVATR WYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT
STLHQLELILETIPPPSEEXRPRQTL DALLPPDTSPEALDLLRRLLVFAPDKRLSATQAL
QHPYVQRFHCP SDEWAREADVRPRAHEGVQLSVPEYRSRVYQMI LECGSSSGTSREKGPE
GVSPSQAHLHKPRADPQLPSRTPVQGP RP RPQSSPGHDP AEHES PRAAKNVPRQNSAPLL
QTALLNGERPPGAKEAPPLTSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV
RVASVQQVPPRLPPEARPGRRMFST SALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL
EGHHV

SEQ ID NO: 177_N28606_H, MOK_H

MKNYKAIGKIGEGTFSEVMKMQLSRDGNYYACKQMKQRFESIEQVNNLREIQALRRLNPH
PNILMLHEVVFD RKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFYT
YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKILT KFKQSRAMNFD FP
FKKSGSIPLLTTNLSPQCLSLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR
KAGFPPEHPVAPEPLSNSCQISKEGRKQKQSLKQEEDRPKRGPAYVMELPKLKLSGVVRL
SSYSSPTLQSVLGS GTNGRVPVLRPLKCIPASKKTD PQDKLPAPQQCRLPTIVRKGG R

SEQ ID NO: 178_AB023153_H, ICK_H

MNRYTTIRQLGDGT YGSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKKNLHA
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLPESAIRNIMYQILOGLAFIHKLG
FFHRDLKPENLLCMGP ELVKIADFG LAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP
IDVWAVGCIMAEVYTLRPLFPGASEIDTIFKICQVLGTPKKTDWPEGYQLSSAMNFRWPQ
CVPNNLKTILIPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS
EKPQKGILERAGPPPYIKVPPPAQPPAKPHTRISSRQH QASQPPLHLTPYKAEVSR TDH
PSHLQEDKPSPLLFP SLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKDSDDWAD
LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVG TGNSAPTQTSYQRRDTPT
LRSAAKQH YLKH SRYLPGISIRNGILSNPGKEFIPPNPWSSSGLSGKSSGTMSVISK VNS
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQRVHLAPIPD PSPGYSSLKAMRPHPGRPFLDT
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179_AA839940_M

SSNNGGMSAEEEIGPGAEPMRGPSLATRDWRDET VGT TDLQQGIDPGAVSPEPGKDHAAG
GPGRTEAGRVSSAAEAAIVLDDSAAPPAPFEHRVVS IKDTLISAGYTVSQHEVLGGGRF
GQVHRCTERSTGLALAAKIIKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT
LIMEYVDGGELFD RITDEKYHLTELDVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

FIGURE 10

QTGHQIKI IDFG LARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL
SGLSPFLGETDAETMNFIVNC SWDFDADTFKGLSEEAKDFVSRLLVKEKSCRM SATQCLK
HEWLNHLPAKASGSNVRLRSQQLLQKYMAQSKWKHFHVVA AVNRLRKFP TCF

SEQ ID NO: 180_AA460132_H

MAAARATTPADGEEPAPEAEALAAARERSRFLSGLLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEEIEGVS
TVRDYIQSTMETKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPEQLNIV
LIDFGLSFISALPEDKGVDLYVLEKAF LSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 181_SGK034_H

QREKVNQGNMPLQSTFLAMDTEEGVEVVWNE LHFGDRKAFAAHEEKIQT VFEQLVLVDH
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTKNHKAMNARAWKRWCTQILS
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKISVWHRIFSNALPDDLRSPIRAEREELR
NLHFFPPEYGEVADGTAVDIFSGMCALEMAVLEIQTNGDTRVTEEA IARARHSLSDPNM
REFILCCLARDPARRPSAHSLLFHRVLF EVHSLKLLAAHCFIQHQYLMPEN VVEEKTAM
DLHAVLAELPRPRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAP
PPEEVQKAKTPTPEPFDSETRKVIQMOCNLERSEDKARWHLTLLL VLEDRLHRQLTYDLL
PTDSAQDLASELVHYGFLHEDDRMKLA AFLESTFLKYRGTQA

SEQ ID NO: 182_AA103218_M SGK034_M

HASAPEYGEVNDGTGFVDIFSGMCALEMAVLEIQANGDTRVTEEA IARARHSLSDPNMR
EFILSCLARDPARRPSAHNLLFHRVLF EVHSLKLLAAHCFIQHQYLMPEN VVEEKTAM
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAP
PEEAQKAKTPTPEPFDSETRKVVQMOCNLERSEDKARWHLTLLL VLEDRLHRQLTYDLLP
TDSAQDLAAELVHYGFLHEDDRMKLA AFLETTFLKYRGTQA

SEQ ID NO: 183_NEK7_H, N34132_H

MSGGAAEKQSSTPGSLFSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT
MDKDSRGAAATTTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH
REETVTATATSQVAQQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPP
ARSGSGGSAKEPQEERSQQQDDIEELET KAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD
TETTVEVAWCELQDRKLT KSERQRFKEEAEMLKGLQHPNIVRFYDSWESTVKGKKCIVLV
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLI IHRDLKCDNIFITGP
TGSVKIGDLGLATLKRASFASVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEY
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIEGCIRQNKDERYSIKDLLNHAFFQ
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESLKKQVEQSSASQ
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQQLQYQQPSISVLSDGTVDGQG
SSVFTESRVSSQQT VSYGF PXHEQAHS TGTVPGHIPSTVQAQSQPHGVYPPSSVQOGIQQ
TAPPQQT VQYSLSTSTSEATTAQPVSQPPAQVLPQVSAGKQSTQGVSVQVAPAEPVAV
AQPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRHE
KTSRPKLRILNVSNKGDRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNDFILAIE
RESFVDQVREIEKADEMLSEDVSVEPEGDQGLQGLKDDYGFSGSQKLEGEFKQPIPA
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN
LSHSASSLSLQQA FSELRRQMTEGPNTAPPNF SHTGPTFPVPPFLSSIAGVPTTAAAT
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSV
SSITIPAVVISITTSPLSQVPTSTSEIIVSSSTALYPSVTVSATSASAGGSTATPGPKPPA
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

FIGURE 1P

HSSTTG LAFSL SAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL
 LPQVPSIPPLVQPVANVPAVQQT LIHSQPQ PALLPNQPHTHCPEVDSDTQPKAPGIDDIK
 TLEEKLRSLFSEHSSSGAQHASVSLETS LVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP
 TNLPLGTVALPVTPVVT PGQVSTPVSTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTL
 PSEQLPPFPGPSLTQSQQPLEDLDAQLRRTLSPEMITVTS AVGPVSMAAPTAITEAGTQP
 QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESS
 VLSSSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTAN
 KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSD
 PEA AFLSRD VDDGSGSPHSPHQLSSKSLPSQNLQSLSNSFNSSYMSSDNESDIEDDLK
 LELRRLRD KHLKEIQDLQSRQKHEIESLYTKLGKVP PAVIIPPAAPLSGRRRRPTKSKGS
 KSSRSSSLGNKSPQLSGNLSGQSAASVLHPQQT LHPPGNI PESGQNQLLQPLKPS PSSDN
 LYSFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184_BCON3_H

MSEGESQTVLSSGSDPKVESSSSAPGLTSVSPVPTSTTSAASPEEEEESEDESEILEESP
 CGRWQKRREEVNRNVPGID SAYLAM DTEEGVEVWNEVQF SERKNYKLQEEKVRVAFDN
 LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKT KKNHKT MNEKAWKRW
 CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINN HVKTCREEQKNL
 HFFAPEYGEVNTVTTAVDIYSFGMCALEMAVLEIQNGESSYVPQEA ISSAIQLLEDPLQ
 REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLAAHCIVGHQHMI PENALEEITKNM
 DTS AVLAEI PAGPGREP VQTLYSQSPALEDKFLEDVRNGIYPLTAFGLPRPQQPQQEEV
 TSPVVPSPVKTPTEPEAEVETR KVVL MQCNIESVEEGVKHHLTLLLKLEDKLNRLHSCDL
 MPNENI PELAAELVQLGFI SEADQSRLTSLLEETLNKFN FARNSTLNSAAVTVSS

SEQ ID NO: 185_AA711829_M

LKQFLKKT KKNHKT MNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK
 IGSVAPDTINN HVKTCREEQKNLHFFAPEYGEVNTVTTAVDIYSFGMCALEMAVLEIQNG
 GESSYVPQEA ISSAIQLLED SLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLLA
 AHCIVGHQHMI PENALEEITKNMDTS AVLAEI PAGPGREP VQTLYSQSPALEDKFLEDV
 RNGIYPLTAFGLPRPQQPQQEEVTSPVVPSPVKTPTEPEAEVETR KVVL MQCNIESVEEG
 VKHHLTLLLKLEDKLNRLHSCDLMPNESIPDLAAELVQLGFI SEADQSRLTSLLEETLNK
 FNFRNSTLNTATVTVSS

SEQ ID NO: 186_AA099102_H

MSSCVSSQPSSNRAAPQDELGGRGSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP
 GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR
 CICPSLPYSPVSSPQSSPRLPRRPTVESHVSI TGMQDCVQLNQYTLKDEIGKSGYGVVK
 LAYNENDNTYYAMKVL SKKKLIRQAAPRRPPRGRTRPAPGGCIQPRGP IEQVYQEIAIL
 KKL DHPNVVKLVEVLDDPNEDHLYMV FELVNQGPVMEVPTLKP LSEDQARFYFQDLIKGI
 EYLHYQKI IHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTPAFMAPESLS
 ETRKIFSGKAKDVWAMGVTL YCFVFGQCPFMDERIMCLHSKI KSQALEFPDQPDIAEDLK
 DLITRMLDKNPESRIVPEIKLHPWVTRHGAELPSEDENCTLVEVTEEEVENS VKHIP S
 LATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP
 PGRHPAPRGGGGSALVRGSPCVESCWAPAGSPARMHPLRPEEAMEPE

SEQ ID NO: 187_5R69_17_2_H

MQEIPQEQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR
 QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGT LRELLDREKDLTLG

FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGTT
REKTDVRVKSTAYLSPQELEDFYQYDVKSEIYSFGIVLWEIATGDI PFQGEEDWLSQW
L

SEQ ID NO: 188_H85811_H
MAPVYEGMASHVQVFSPTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS
QPATTTVSTSLPVPNPSPLYEQTIVFPGSTGHI VVTSASSTSVTGQVLGGPHNLMRRSTV
SLLDITYQKCGLKRKSEI ENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS
EGDYQLVQHEVLCSMTNTYEVLEFLGRGTFGQVVKCWKRGTEI VAIKILKNHPSYARQG
QIEVSILARLSTESADDYNFVRAYECFQHKHNTCLVFEMLEQONLYDFLKQNKFSPLPLKY
IRPVLQQVATALMKLKSGLIHADLKPENIMLVDPSPRPYRVKVIDFGSASHVSKAVCST
YLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP
AEYLLSAGTKTTRFFNRDTSPLYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN
MTTDLEGSMDLVEKADRRREFIDLLKMLTIDADKRITPIETLNHPFVTMTHLDDFPHSTH
VKSCFQNMIEICKRRVNMYPDVTNQSCTPFITHVAPSTSTNLMTFNNQLTTVHNQPSAASM
AAVAQRSMPLQTGTAQICARPDFFQALIVCPPGFQGLQASPSKHAGYSVRMENAVPIVT
QAPGAQPLQIQPGLLAQQAWPSGTQQIILLPPAWQQLTG VATHTSVQHATVIPETMAGTQQ
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAAQPLNVGVAHV MRQQPTSTTSSRKSQKH
QSSVRNVSTCEVSSSQAISSPQRSKRVKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT
RERQRQTIVIPDTPSPTVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDS PYS
DSSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDSLV
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITYRQQRPGPHFQQQQPLNLSQAQQHI
TTDRTGSHRRQQAYITPTMAQAPYSFPHNSPSHGTVHPHLAAAAAAHLPTQPHLYTYTA
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQVPVSMGPRVLPSPTIHPSQYPAQF
AHQTYISASPASTVYTGYP LSPAKVNQYPYI

SEQ ID NO: 189_DYRK3_H
MMIDETKCPPCSNVLCNPSEPPPPRRRLNMTAEQFTGDHTQHFLDGGEMKVEQLFQEFGNR
KSNTIQSDGISDSEKCSPTVSQKSSDCLNTVKSNSSSKAPKVPLTPEQALKQYKHHLT
AYEKLEIINYPEIYFVGPNAKKRHGVIGGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII
GKGSFGQVARVYDHKLQYVALKMVRNEKRFHRQAABEIRILEHLKKQDKTGSMNVIHML
ESFTFRNHVCMFAFELLSIDLIELIKKNKFQGFVSVQLVRKFAQSILQSLDALHKNKIIHCD
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF
RCILAELLTGQPLFPGEDEGDQLACMELLMGPPPKLLEQSKRAKYFINSKGIPRYCSVT
TQADGRVVLVGGRRRGKKRGPFGSKDWGTALKGCDDYLFIEFLKRCLHWDPSARLTPAQ
ALRHPWISKSVPRLTTIDKVSGKRVNPAFAQGLGSKLPPVVGIANKLKANLMSETNG
SIPLC SVLPKLIS

SEQ ID NO: 190_AA589241_M DYRK3_M
TRPELLGMPPQKLEEQSKRAKYFINSGLPRYCSVSTQTDGRVVLGGRSRRGKKRGPFG
SKDWATAKGC GDYLFIEFLKRCLQWDPSARLTPAQALRHPWISKSTPKPLTMDKVPGKR
VVNPTNAFQGLGSKLPPVVGIA SKLKANLMSETSGSIPLC SVLPKLIS

SEQ ID NO: 191_5R72_16_2_H
MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKEPPEINLVLY
PQGLTGEEVYVKVDLRVKCPPTYPDVVP EIELKNAKGLSNESVNLLKSRLEELAKKHCGE
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQORLLEAKRKEEQEQREILHEIQ
RRKEEIKEEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHGGSPDFVGN GKHR
ANSSGRSRRERQYSVCNSEDSPGSCIEILYFNMGSPDQLMVHKGKCI GSDEQLGKLVYNAL
ETATGGFVLLYEWVLQWQKKMGPF LTSSQEKEKIDKCKKQIQGTETEFNSLVKL SHPNVVR

FIGURE 1R

YLAMNLKEQDDSI VVDILVEHISGVSLAAHLSHSGPI PVHQLRRYTAQLLSGLDYLSHSNS
 VVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD
 VWRLGLLLLLSLSQGQECGEYPVTIPSDLPADFDLKKCVCLDDKERWSPQQLLKHSFIN
 PQPKMPLVEQSPEDSGGQDYVETVIPSRLPSAAFFSETQRQFSRYFIEFEELQLLGKGA
 FGAIVKVNKLGDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVRYNNAWIERHE
 RPAGPGTPPPDSGPLAKDDRAARGQPASD TDGLDSVEAAAPPPILSSSVIEWSTSGERSAS
 ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSESDIIFDNEDENSKSQNQDEDCNEK
 NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH
 EKGMIHRDLKPVNIFLSDDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTG
 MVGTALYVSPVQGSTKSAYNQVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPSTP
 KFPEDFDDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPQMEESSELHEVLHHTLT
 NVDGKAYRTMMAQIFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIRIFKRHGA
 VOLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE
 RVFRPRKLD RHPKELLECAFDIVTSTTNSFLPTAEIITYIYEIIQEFPALQERNYSIYL
 NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKF
 IEQKGLDQLMPTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK
 VQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIADK
 ISAAVLNMEESVTISSCDLLVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
 EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETTELVDHVLQKLRTKVTDERNG
 REASDNLAQNLKGSFSNASGLFEIHGATVVPISVLAPEKLSASTRRRYETQVQTRLQT
 SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
 DEIYNIKVEKKVSVLFLYSYRDDYYRILF

SEQ ID NO: 192_R43524_H, HRI_H

MLGGNSGVRKREEEGDAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP
 FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLLSSFTCSDEFSSRLHH
 NRAITHLMRSAKERVRQDPCEDISRIQKIRSREVALEAQTSRYLNEFEELVILGKGGYGR
 VYKVRNKL DGQYYAIKKILIKGATKTVMKVLREVKVLAGLQHPNIVGYHTAWIEHVHVI
 QPRADRAAIELPSLEVLSDQEEDREQCGVKNDSSSSSIIFAEPTPEKEKRFGESDTENQ
 NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQPLLRN SHLEESFTSTEE
 SSEENVNFLGQTEAQYHMLMLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT
 KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN
 GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSGLGVLLLELFQPFQTEMERAEVLTGL
 RTGQLPESLRKRCVPQAKYIQHLTRRNSSQRPSAIQLLOSELFQNSGNVNLTLMKII EQ
 EKEIAELKKQLNLLSQDKGVRDDGKDDGGVG

SEQ ID NO: 193_17000057519457_H

MAAARATTPADGEEPAPAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
 HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEIEGVS
 TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
 LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
 EVRLRGRKRSMVG

SEQ ID NO: 194_AA013524_M

LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRTVQEARALLRCRRAGIA
 APVVFFVDYASNCLYMEIEEDSVTVRDYIQSTMETEKDPQCLLDLARRMGQVLAMHDQD
 LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFVSGLPEDKGVDLYVLEKAFLSTHPHTETA
 FEAFLKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

FIGURE 1S

SEQ ID NO: 195_17000139801197_H, IRAKM_H
 MAGNCGARGALSAHTLLFDLPPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK
 YVDQKGSGTRELLWSWAQKNKTIGDLLQVLQEMGHRRRAIHLITNYGAVLSPSEKSYQEGG
 FPNILFKETANVTVDNVLIPHENEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY
 RVEIQNLTYAVKLFKQEKMQCKKHWKRFLESEVLLLLFHHPNILELAAYFTETEFCL
 YPYMRNGTLFDR LQCVD TAPLPWHIRIGILIGISKAIHYLHNVPSCSVICGSISSANIL
 LDDQFQPKLTDFAMAHFRSHLEHQSTINMTSSSSSKHLWYMPEEYIRQGLSIKTDVYSF
 GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRGLDSCSLF LDKKVP PCPRNFS AKLFC
 LAGRC AATRAKL RPSMDEV LNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE
 DDESQNNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSCE
 ESWF PKYIVPSQDLR PYKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196_AA840598_M IRAKM_M
 MWKRFLSEVLLLLFRHPHILELAAYFTETEKLC LVYPYMSNGTLFDR LQCTNGTTPLSW
 HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ
 SSTINMTGGGRKHLWYMPEEYIRQGR LSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR
 DLLMELMEKRGLDSCSLF LDRKI PPCPRNFS AKLFS LAGRCVATKAKLRPTMDEV LSSLE
 STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHSVPPKEVLGTDRVTQK
 TPFECSQSEVTF LGLDRNRGNRGSEADCNPSSSHEECWSPELVAPSQDLSPTVISLGSS
 WEVPGHSYGSKPMEKRCSSGLFCSEHEQSKKQ

SEQ ID NO: 197_AA088547_H
 MASAVRGSRPWPR LGLQLQFAALLLGTLS PQVHTLRPENLLLSTLDGSLHALSKQTGDL
 KWTLRDDPVIEGPMYVTEMAFLSDPADGSLYILGTQKQQGLMKLPFTIPELVHASPCRSS
 DGVFYTG RKQDAW FVVD PESGETQMTLTTEGPSTPRLYIGRTQYTVTMHDP RAPALRWNT
 TYRRYSAPPMDGSPGKYMSHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTW HQDGL
 RQLPHLT LARDTLHFLALRWGHIRLPASGPRDTATLFSTLDTQLLMTLYVGKDETFYVS
 KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYPGSGVALPSQWLLI
 GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK
 TPDSYLG LGPQDLLAASLTAVLLGGWILFVMRQVVEKQQETPLAPADFAHISQDAQSLHS
 GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRA
 VAVKRL LREC FGLVRREVQLLQESDRHPNV LRYFCTERGPQFHYIALELCRASLQEYVEN
 PDLDRGGLEPEVVLQQLMSG LAHLHSLHIVHRDLKPGN ILITGPD SQGLGRVVLSDFGLC
 KKLPA GRCSFSLHSGIPGTEGWMAPELLQLLPDSPTS AVDIFSAGCVFYVLSGGSHPF
 GDSLYRQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAPFFWSR
 AKQLQFFQDVSDWLEKESEQEPLVRALEAGGCAVVRDNWHEHIS MPLQTDLRKFRSYKGT
 SVRDL LRAVRNKKH YREL PVEVRQALGQVPDGFVQYFTNRFPRLLLH THRAMRSCASES
 LFLPYYPDPDEARRPCPGATGR

SEQ ID NO: 198_HGP_6644466
 MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRS PRGLSHSP
 WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE
 KSLNDLIEERYKASQDPFPAAILKVALNMARG LKYLHQEKLLHGD I KSSNVVIKGD FE
 TIKICDVGS LPLDENMTVTDPEACYIGTEPWKPKEAVEENGVI TDKADIFAFGLTLWEM
 MTL S I PHINLSNDDDDDKTFDESDFDEAYYAALGTRPPINMEELDESYQKVIELFSVC
 TNEDPKDRPSAAHIVEALETDV

SEQ ID NO: 199_AA449542_M
 SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKNLNHPNIGYRAFTEASDGSL
 CLAMEYGGESLNDLIEERNKDSGSPFPAAVILRVALHMARG LKYLHQEKLLHGD I KSS

FIGURE 1T

NVVIKGD FETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV
 AFGLTLWEMMTLCIPHVNLPDDVDDEDAFDESDFDDEAYYAALGTRPSINMELDDSYQK
 AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200_5R57_10_2_M TESK2_M
 LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201_AA232253_H
 MSSLGASFVQIKFDDLQFFENC GGGSFGSVYRAKWISQDKEVAVKLLKIEKEAEILSVL
 SHRNI IQFYGVILEPPNYGIVTEYASLGSLDYINSNRSEEMDMDHIMTWATDVAKGMHY
 LHMEAPVKVIHRDLKSRNVVIAADGV LKICDFGASRFHNHTTHMSLVGTFPWWAPEVIQS
 LPVSETCDTYSYGVVLWEMLTREVFPKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH
 QCWEADAKKRPSFKQII SILESMSNDTSLPDKNSFLHNKAWE RCEI EATLERLKKLERD
 LSFKEQELKERERRLKMWEQKLTEQSNTPLPSFEIGAWTEDDVYCWVQQLVRKGDSSAE
 MSVYASL FKENNITGKRLLLLLEEDLKDMGIVSKGHI IHFKSAIEKLTHDYINLFHFPPL
 IKDSGGEPEENEKIVNLELVFGFHLKPGTGPDCKWKMYMEMDGDEIAITYIKDVTFNT
 NLPDAEILKMTKPPFVMEKWIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ
 DEVKAVQLAIQTLFTNSDGNPGSRSDSSADCQWLDTLRMQIASNTSLQRSQSNPILGSP
 FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSSPTQYGLTKNFSSLHLNSRDSGFS
 SGNTDTSSEGRYSDRSRNKYGRGSI SLNSSPRGRYSGKSQHSTPSRGRYPGKFYRVQS
 ALNP HQSPDFKRSRDLHQPN TIPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP
 SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202_AI375137_H
 MGNYKS RPTQTCTDEWKKKVSES YVITIERLEDDLQIKEKELTEL RNIFGSDEAFSKVNL
 NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL
 LHSGADIQQVGYGGLTALHIATIAGHLEAADVLLQHGANVNIQDAVFFTPLHIAAYYGHE
 QVTRLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVP LH
 FCSRFGHHDIVKYLLOSDLEVQPHVNIYGDTPHLHLACYNGKFVAK EIIQISGTESLTK
 ENIFSETAFHSACTYGKSIDL VKFLLDQNVININHQGRDGHTGLHSACYHGHIRLVQFLL
 DNGADMNLVACDPSRSSGEKDEQTCLMWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG
 GDGSYVSVPSPLGKIKSMTKEKADILLRAGLP SHFHLQLSEIEFHEIIGSGSFGKVYKG
 RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCV IQFVGACLN DPSQFAIVTQ
 YISGGSLSFLLHEQKRILDQSKLIIAVDVAKGMEYLHNLTQPIIHRDLNSHNILLYEDG
 HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT
 GEIPFAHLKPAAAAAD MAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE
 ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA
 LSQSAGQYSSQGLSLEEMKRSLQYTPIDKYGYVSDPMSSMHFHS CRNSSSFEDSS

SEQ ID NO: 203_H97685_H
 MESERSPLYRQLIDLGYLSSSHWNC GAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRL
 VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE
 MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEVGTREIKCCIRQIQELIISR LNQA
 VANKLISSVDYLRESFVGTLERCLOSLEKSQDVSVHITSNYLKQILNAA YHVEVTFHSGS
 SVTRMLWEQIKQIIQRITWVSPPAITLWKRKVAQEAIESLSASKLAKSICSQFRTRLNS
 SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHAPRLARLSLESRS LQDVLLHRKP KLG
 QELGRGQYGVVYLCDNWGGHFP CALKSVVPPDEKHWNDLAL EFHYMRSLPKHERLVDLHG
 SVIDYNYGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH
 RDIKLNVL LDKQNRAKITDLGFCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK
RPLLGLIVQPMQLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204_W20810_M

DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSLIRETVCDRQSRPPLTELPPGSPET
PGLEKLKELMIHCWGSQSENRPFSQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG
RNLSAREPSQRGTEMDCPRETMVSKMLDRLHLEEPSGVPVPGKCPERQAQDTSVGPATPAR
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHQQRNQGDGRHGTPWYPWTPPNPMTGP
PALVFNNCSEVQIGNYNLSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205_AA744236_H

MGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYKRENEDKVNKAAKHLKTL
RHPCLLRFLSCTVEADGIHLVTERVQPLEVAETLSSAECAGIYDILLALIFLHDRGHL
THNNVCLSSVFSVEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPFTT
LPECHGHARDAFSFGTLVESLLTILNEQVSADVLSSFQOTLHSTLLNPIPKCRPALCTLL
SHDFFRNDFLEVNFLLKSLTLKSEEEKTEFFKFLDRVSLSEELIASRLVPLLLNQLVF
AEPVAVKSFLPYLLGPKKDHQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLISH
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSVDKNTSEDSNFSSSKKSEEPDWSE
PEEPENQTVNIQIWPREPCDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV
TSGEQKPIPALSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG
LGEEFTIQVKKKPKVDPEMDWFAFMIPEIKPSAAFLILPELRTMVPKDDVSPVMQFSS
KFAAAEITEGEAEGWEEEGELNWEDNNW

SEQ ID NO: 206_AI052250_H

MESMLNKLKSTVTKTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE
VAVFVFDKKLIDKYQKFEKDQIIDSLKRGVQQLTRLRHPRLTLVQHPLEESRDCLAFCTE
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT
PENIILNKSGAWKIMGDFCVSSTNPSEQEPKFPCKEWDPNLPSLCLPNPEYLAPEYILS
VSCETASDMYSLGTVMYAVFNKGKPIFEVKNQDIYKSFSRQLDQLSRLGSSSLTNIPEEV
REHVKLLLNVTPTPVRPDADQMTKIPFFDDVGAVTLQYFDTLFQRDNLQKSQFFKGLPKVL
PKLPKRIVQRIPLCLTSEFVNPDMPFVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ
EPIQILLIFLQKMDLLLTTPDEIKNSVLPVYRALEAPSIQIQELCLNIIPTFANLID
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207_AA278842_H

MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEEQTQV
AKAAFKRFKTLRHPNIIAYIDGLETEKCLHVTEAVTPLGIYKARVEAGGLKELEISWG
LHQIVKALSFLVNDCSLIHNNVCMMAVFVDRAGEWKLGGLDYMYSAQNGGGPPRKGIPE
LEQYDPPELADSSGRVVREKWSADMWRLGCLIWEVFNGLPRAAALRNPGKIPKTLVPHY
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS
LDAFPEDFCRHKVLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS
TDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVHGFLLDTPAIREQTVKSMLLLAPKLN
EANLNVELMKHFAARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPF
APSRVAGVLGFAATHNLYSMNDCAQKILPVLCLTVDPEKSVRDQAFKAIRSFLSKLESV
SEDPTQLEEVEKDVAASSPGMGGAASWAGWAVTGVSSLTSLIRSHPTTAPTETNIPQ
RPTPEGVPAPAPTVPATPTTSGHWETQBEDKDTAEDSSSTADRWDDEDWGSLEQEAESVL
AQQDDWSTGGQVSRASQVSNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEPDPDGR
LASEYNWGGPESSDKGDPFATLSARPSTQPRPDSWGEDNWEGLTDSRQVKAELARKKRE
ERRREMEAKRAERKVAKGPMKLGARKLD

FIGURE 1V

SEQ ID NO: 208_AA599286_H

MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD
PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLWS
ADLGPDKYLSDKDFQCLIKLLPSC LHPYIYRVTFATANESSALLIRMFNEKGTLDLIYK
AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGH LHASNVMLDGD
CRLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP
PAPSMVAVVLESTLSCEACKNGMPTISRLLQMP LFS DVLLTTSEKPQFKIPTKLKEALR
IAKECIEKRLIEEQQIHQHRRLTRAQSHHGSEERKKRKILARKKSKRSALENSEEHSA
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEAPAQLS
SQAVNGMSRGALLSSIQNFQKGT LRKAKPVITVLRSSAEASCLHLEGKVL FYSYSP LPPN
YPLPGKVIAEPVQPQTVLFCRCSCCKQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209_AA425725_H

MSASTGGGGSDSGSGSGSSSSSSQASCGPSSGSELALATPVPQMLQGLLGSDDEEQEDPKD
YCKGGYHPVKIGDVFNGRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVK SAGHYTETA
VDEIKLLKCVRSDSPDPKRETIVQLIDDFRISGVNGVHVC MVLEV L GHQLLKWIIKSNY
QGLPVPVCVKSIVRQVLHGLDY LHTKCKI IHTDIKPENILLCVGDAYIRRLAAEATEWQQA
GAPPPSR SIVSTAPQEVLTGKLSKNKRKKMRKRKQKRLLEERLRDLQRLEAMEAATQA
EDSGRLRDGSGSGSTSSSGFSGSLFSPASC SILSGSSNQRETGGLLSPSTPFGASNLLVNP
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGPADIWSTACMAF
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDI PP AFALSGRYSREFFNRRGELRHIHN
LKHWGLEYEVLMEKYEWP LEQATQFSAFL LPMMEYIPEKRASAADCLQHPWLNP

SEQ ID NO: 210_SGK022_H

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ
IVRTL DHKNIIQVYEMLESADGKICLVME LAEGGDVFD CVLNGG PLPESRAKALFRQMV E
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFAKVL PKSHRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGV SFPTHLSISADCQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 211_AA060026_M SGK022_M

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ
IVRTL DHKNIIQVYEMLESADGKIYLVME LAEGGDVFD CVLNGG PLPESRAKALFRQMV E
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFAKVL PKSRRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGV SFPTHLGISTECQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 212_AA399669_H

MGKGDVLEAAPT TTTAYHSLMDEYGYEVGKAIGHGSGSVYEA FYTKQKVMVAVKII SKKK
ASDDYLNKFLPREIQVMKVL RHKYLINFYRAIESTSRVYIIILELAQGGDVLEWIQRYGA
CSEPLAGKWFSQ LTLG IAYLHKSIVHRDLKLENLLLDK WENVKISDFGFAKMVPSNQPV
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLPF
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213_AA758539_H

MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE
MDILATVNHGSI IKTYEIFETSDGRIYIIMELGVQGD LLEFIKCQ GALHEDVARKMFRQL
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

FIGURE 1W

YAAPEVLQSIPIYQPKVYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQKEHRVDFPRSKN
LTCECKDLIYRMLQPDVSQLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHISGAEVGKAST

SEQ ID NO: 214_AA883975_H
MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE
LSILRGVRPHIVHVFIEVCNGKLYIVMEAAATDLLQAVQRNGRIPGVQARDLFAQIA
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRAHGYPDLSSTTYCGSAAYASP
EVLLGIPYDPKKYDVWSMGVVLVYVMVTGCMFDDSDIAGLPRRQKRGVLYPEGLELSERC
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215_AA905446_H
VGRQETGVRRWAFILCQIPSPPLTSSEFIQRFLPRELQIVRTL DHKNI IQVYEMLESADG
KICLVMELAEGGDVFDVLCVNGGPLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALL
QGFNLKLTDFGFAKVLPKSHRELSQTF CGSTAYAAPEVLQGI PXKMLWQQQKGVSPFTHL
SISADCQDLLKRLLEPDMILRPSIEEVS WHPWLAST

SEQ ID NO: 216_H29974_H
YSLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAEPCYLWFMVMEFCEGG
DLNQYVLSRRPDPATNKS FMLQLTSAIAFLHKNHIVHRDLKPDNILITERSGTPILKVAD
FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYMAPEVWEGHYTAKADIFALG
IIIWAMIERITFIDSETKKELLGTYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG
IKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 217_AA498104_M H29974_M
PLLLPPPPAAMETGKENGARRGTS PERKRRSPVQVRLCEKLRPAAQAMPAGAEVPGEA
FLARRRPDGGGVDV PARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE
LALAEFWALTSLKRRHQNVQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL
GYAEPCYLWFMVMEYCEGGDLNQYVLSRRPDPATNKS FMLQLTSAIAFLHKNHIVHRDLK
PDNILITERSGTPILKVADFGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYM
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKELLGTYIKQGT EIVPVGEALLE
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 218_AA215311_H
MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI
KSQHPNVIHLEECILQKGMVQKMSHGSNSSLYLQLVETSLKGEIAFDPRSAYYLWFMVD
FCDGGDMNEYLLSRKPNRKTNTSFMLQLSSALAFHKNQI IHRDLKPDNILISQTRLDTS
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTD FYMAPEVWEGHYTAKADI
FALGIIIWAMLERITFIDTETKKELLSYVKQGT EIVPVGEALLENPKMELLI PVKKKSM
NGRMKQLIKEMLAANPQDRPD AFELELRLVQIAFKDSSWET

SEQ ID NO: 219_AA018361_H
MRAAFPAGGAGGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPPRLDGFILT
ERLGS GTYATVYKAYAKD TREVVAIKCVAKKSLNKASVENLLTEIEILKGIRHPIVQL
KDFQWSDNIYLIMEFCAGGDL SRFIHTRRILPEKVARVFMQQLASALQFLHERNISHLD
LKPQNILLSSLEKPHLKLADFGFAQHMS PWDEKHVLRGSPLYMAPEMVCQRQYDARVDLW
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLQLLERDPSR
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALSLYCKALDFFVPA

FIGURE 1X

LHYEVDQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARKPRLL
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSRAGGGSCFTLRFRTSWPELN
T

SEQ ID NO: 220_AA311714_H
MENFILYEEIGRGSKTVVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIIVT
FHEWYETSNHLWLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL
KFSNFCIAKVEGENLEEFFALVAAEEGGGDNGENVLKKSMSRVKGSPPVYTAPEVVVRGAD
FSISSDLWSLGCILLYEMFSGKPPFFSESSELTEKILCEDPLPPIPKDSSRPKASSDFIN
LLDGLLQRPDQKRLTWTRLLQHSFWKAFAGADQESSVEDLSLSRNTMECSGPQDSKELL
QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPTPTSTAVEV
SPGEDMTHCSPOKTSPLTKITSGHLSQQDLESQMRELIYTDSDLVVTPIIDNPKIMKQPP
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV
AGHQEVATRLLHSPLFQLLIQHRLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS
SIGIGILNCLVQHSTPVPRQCLVYV

SEQ ID NO: 221_SGK384_H
SLAHVLRARQILTEPEVRDYLRLVSGRLRYLHQRCILHR

SEQ ID NO: 222_AA210451_M SGK384_M
MGQQHGTRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPRSTADSRRCPPGYFR
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH
GLQMLKSLQSEHVTVLVGYCEEDGTILTEYHPLGSLSNLEETLNLSKYQDVNTWQHRLQL
AMEYVSIINYLHHSPLGTRVMCDSDNLPKTLQYLLTSNFSIVANDLDALPLVDHDSGVV
IKCGHRELHGDVFAPEQLWPYGEDTPFQDDLMPSYNEKVDIWKIPDVSSFLLGHVEGSDM
VRFHLLFDIHKACKSQIPAERPTAQNVLDAYQRFVHSLRDTVMSQTKEML

SEQ ID NO: 223_SGK071_2_H
EVVAVQMMVECMDDHYASQALEELMPLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALLEYLHHLDIHRNLKPSNIIILISSDH
CKLQDLSSNVLMTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC
SFMGDTEAMHLRKSRLRQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD
VVHITFLRGSFKSSCVSLTLHRQMVPASITDMLLEGNVASILGDAGDTKGERALKLLSMA
LASYCLVPEGSFLMPLALLHMHQWLSCDQDRVPGKRDFAISLGLKGLGPIPKGLPWPP
ELVEVVVTMELHDRVLDVQLCACSLLLHLGLQALVHHPEAKAPCNQAITSTLLSALQSH
PEEEPLLVMVYSLLAITTTQESSESLSEELQAGLLEHILEHLNSSLERDVCASGLGLLW
ALLLDDPILALQRPKRKRAPNHGKPGKPNPASTQSIIVNKAPLEKVPDLISQVLATYPA
DGEMAEASCGVFWLLSLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKV
SELAAFKVVVQEEGGSGLSLIKETYQLHRDDPEVVENVGMMLLVHLASYEELPELVSSSM
KALLQEIKERFTSSSLVSDSSAFSKPGLPPGGSPQLGCTTSGGLE

SEQ ID NO: 224_AA118352_M SGK071_M
EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL
KPILKTMEEKQIPGTDVYYLLLPFMLHINPSDRLAIKDVMQVTFMSNSFKSSSVALNMQR
QKVPIFITDVLLEGNMANILGSWLCASFVNDNRHCDSGIGSQRLGFDQSVSWTEHPLKD
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEVISIIKQHGRILDILLSTCSLL
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISQGGQISEEL
EEEGFLQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVLLLRSIQLCPGRVLLVNNAFRGLASLAK

FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLEQEDQLEPPAGQEAPLOGEPLFRP

SEQ ID NO: 225_018653.9_H

GRGRGAGHARGLRGPAGRRAEPFRSLSRPGPGPGSRAGPAGRGEGSDAAPAGGSGRGFL
RLLPAGLRPQORALRSGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG
GPGPGAGRPERRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA
ALRNVSQAQYMGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA
HKLLKEMVLLERLRHPNVQLYGYCYQDSEIPDTLTTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDIVNATGE
LAWGVDETALQLEKVLHLRSGQYLQNSTASSSTEYQCI PDSTIPQEDYRCWPSYHHGSC
LLSVFNLAEAVDVCESHAQCRAFVVTNQTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226_AA396601_M

TRPGCAALRNVSQAQYVGSYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGARRG
CYRLAAHKLLKEMVLLERLRHPNVQLYGYCYQDSEIPDTLTTITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLDFRPRQFVLVNGELKVTDLDDARVEETPCT
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDIVNATGE
LAWGVDETALQLEKVLHLRSGQYLQNSTSSRAEYQRI PDSAITQEDYRCWPSY
HHGGCLLSVFNLAEAIDVCESHAQCRAFVVTNQTWTGRKL VFFKTGWNQVVPDAGKTTY
VKAPG

SEQ ID NO: 227_VRK3_H

MISFCPDCGKSIQA AFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP
KKVKWSSTVTSRPLSLFSDGDSSESEDTLSSSERSKSGSGSRPPTPKSSPQKTRKSPQVTR
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLSFQTRDNQGIL
YEAAPTSTLTCDSGPQKQKFSKLDKDAKDGRLFNEQNFFQRAAKPLQVNWKKLYSTPLLA
IPTCMGFGVHQDKYRFLVPSLGRSLQSALDVSPKHVLSERSVLQVACRLDDALEFLHEN
EYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFI SMD
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP CGH
WIRPSETLQKYLKVVMAITYEEKPPYAMLRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228_S71575_M VRK3_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSALDDNPKHVVSERCVLQVACRLDDALEYLHEN
EYVHGNLTAENVFVN PEDLSQVTLVGYGFTYRYCPGKGHVAYKEGSRSPHDGDLEFI SMD
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTTEKITRQKQKYLDSPERLVGLCGR
WNKASETLREYLKVVMA LNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQ MVP

SEQ ID NO: 229_AA45427_H

MGHALCVC SRGTVIIDNKRYLFIQKLGE GGF SYVDLVEGLHDGHFYALKRILCHEQQDRE
EAQREADMHR LFNHPN IRLVAYCLRERGAKHEAWLLLPFFKRGT LWNEIERLKDKNFL
TEDQILWLLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLM DLGSMNQACIHVEGS
RQALTLDWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGC VLYAMMFEGGPYDMVFQ
KGDVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRP H I P L L L S Q L E A L Q P P A P G Q
HTTQI

SEQ ID NO: 230_H05721_H

MAVRQALGRGLQLGRALLLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEP RRVG
LGLPNRLRFFRQSVAGLAARLQRQFVVRWGCAGPCGRAVFLAFGLGLGLIEEKQAESRR

FIGURE 1Z

AVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRL E EYLI GQSIGKGCSAAVYEATMPTLPQ
 NLEVTKSTGLLPGRPGTSAPGEGQERAPGAPAFPLAIKMMWNI SAGSSSEAILNTMSQE
 LVPASVALAGEYGAVTYRKS KRGPQLAPHNI I RVLRAFTSSVPLLP GALVDYDPVLP
 SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTSPRLAAMMLLQ LLEGVDHLVQOGIAH
 RDLKSDNILVELDPDGPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST
 ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFFYQGQKAHLESRSYQEAQLPALPESVPP
 DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMGVWLLQQAATLL
 ANRLTEKCCVETKMKMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231_AI086865_H

MEKYERIRVVGRGAFGIVHLCLRKADQKLVIIKQIPVEQMTKEERQAAQNECQVLKLLNH
 PNVIEYYENFLEDKALMIAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQIILLALHHVH
 THLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSTPCYISP ELCEGKPNQKSDIW
 ALGCVLYELASLKRAFEANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP
 PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQRGIIIMTFGSGSNGCLGHGS
 LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEP LLSIDLGTAHSAAVTGEEDL
 GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPDKCCWRHKQCTGHI IYPFASDCV
 RHSLHLHSVNHNCNSRLKDSSSEDSSSRGAGPTCSHVIESPCFELTPEEEHVERFRYGW
 CKSYRPVSVAVIHHPHYHECGADDLNXXKKRKRRRRKS KPP IPTQVGPATASPD LGTSMAT
 GTPDSTAPITIWRSSEPTGKGQGSKVIKKVKKKKEKEKDEEMDEKAKLKKKAKKGQLTK
 KKSVPKLEPSPDPVSRSL SARQLARMESSPESREELESEDSYNGRGQGELSSSEDI VESS
 SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232_AA836348_H

MSVLGEYERHCDSINSDFGSES GCGDSSPGPSASQGPRAGGGAEEQEELHYIPIRVLGR
 GAFGEATLYRRTEDDSL VVWKEVDLTRLSEKERRDALNEIVILALLQHDNIIAYYNHFM D
 NTTLLIELEYCNGGNLYDKILRQKDKLFEEEMVVWYLFQIVSAVSCIHKAGILHRDIKTL
 NIFLTKANLIKLDYGLAKKLNSEYSMAETLVGTPPYMSP ELCOGVKYNFKSDIWAVGCV
 IFELLTLKRTFDATNPLNLCVKIVQGIRAMEVDSSQYSLELIQMVHSCLDQDPEQRPTAD
 ELLDRPLLRKRRRSSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG
 NTHFAVVTVKEKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLQGKAIRQVSCGDDF
 TVCVTDEGQLYAFGSDYYGCMGVDKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVVLT R
 NKEVYSWGCGEYGRGLDSEEDYYTPQKVDVPKALIIVAVQCGCDGTFLLTQSGKVLACG
 LNEFNKLG LNLQCMSGIINHEAYHEVPYTTSFTLAKQLSFYKIRTIAPGKTHTA AIDERGR
 LLTFGCNKCGQLGVGN YKKRLGINLLGGPLGGKQVIRVSCGDEFTIAATDEKVLNSKTIR
 SNSSGLSIGTVFQSSSPGGGGGGGGEEEDSQQESETPDPSGGFRGTMEADRGMEGLISP
 TEAMGNSNGASSSCPGWLRKELENAEFI PMPDSPSPLSAAFSESEKDTLPYEELQGLKVA
 SEAPLEHKPQVEASVTELFAPESQLV TSAESCSNLCWEGNTTDS SCVCVQLSAGGG

SEQ ID NO: 233_R86668_H, MKK6_H

MNLLLSYRDVQDYS AIIELVETLQALPTCDVAEQHNVC FHYTFALNRRNRPGDRAKALSV
 LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYHWYRKAFDVEPSLHSGIN
 AAVLLIAAGQHFEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLG AQILANDPTQV
 VLAAEQLYKLNAPIWYLVSMETFLLYQHFRPTPEPPGGPPRAHFWLHFL LQSCQPFKT
 ACAQGDQCLVLVLEMNKVLLPAKLEVRGTDVPSTVTL SLLPETQDIPSSWTFPVASICG
 VSASKRDERCCFLYALPPAQDVQLCFPSVGHCQWFCGLIQAWVTNPDSTAPAEAEAGAGE
 MLEFDYEYTETGERLVLGKGTYG VVYAGRDRHTRVRIAIKEI PERDSRFSQPLHEEIALH
 RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRSVWG PLKDNESTISFYTRQILQ
 GLGYLHDNHI VHRDIKGDNLINTFSGLLKI SDFGTSKRLAGITPCTETFTGT LQYMAPE
 IIDQGRPGYGKAADIWSLGCTVIEMATGRPPFHELGS PQAAMFQVGM YKVHPPMPSSLSA

FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN
STTQSQTFFPCPQAPSQHPPSPPKRCLSYGGTSQLRVPEEPAAEEPASPEESSGLSLLHQE
SKRRAMLAHVLEQELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ
ELRALQGRRLAQGLGPALLHRPLFAFPDAVKQILRKRQIRPHWMFVLDLSLSRAVRAALG
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR
EILAGKEREYQALVQRALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM
LLNHSFTLHTLLTYATRDDLITYTRIRGGMVCRIWRAILAQRAGSTPVTSGP

SEQ ID NO: 234_PAK6_H

MFGKKKKKIEISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT
PIQLAPMKTIVRGNKPKETSINGLLEDFDNI SVTRSNLSRKESPTPDQGASSHGPGHA
EENGFIITFSQYSSSEDTTADYTTKEYREKSLYGGDDLPYYRGSHAQKQNGHVMKMKHGEA
YYSEVKPLKSDFAFSADYHSHLDSLSKPSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA
GTSGCSKESLAYSESEWGPSLDDYDRRPKSSYLNQTSPOPTMRQRSRSGSGLQEPMPFG
ASAFKTHPQGHSYNSYTYPRLSEPTMCIPKVDYDRAQMVLSPLSGSDTYPRGPAKL PQS
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSQYISTASYLSSLSLSSSTYPSPSWGSSS
DQQPSRVSHEQFRAALQLVVSPGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM
DLRKQORRELLFNEVVIMRDYHHDNVDMYSSYLVGDELWVVMFLEGALTDIVTHTRM
NEEQIATVCLSVLRALSYLHNQGVHRIKSDSILLTSDGRIKLSDFGFCQVSKEVPKR
KSLVGTPYWMapevisrlpygtevdiwslgimviemidgepppfnepplqamrrirdslp
PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235_SURTK106_H

MNDRNEIQMEAKLQSLTIIAQEILCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI
LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIEKQYEVII VPTLLVTIFLILLGVILWL
FIREQRTQQQRSGPQGIAPVPPPRDLSEAGHGNNVALPLKETSVENFLGATTPALAKLO
VPREQLSEVLEQICSGSCGPIFRANMNTGDPSKPKSVILKALKEPAGLHEVQDFLGRIQF
HQYLKGKHNVLVQLEGCTEKLPLYMVLEDVAQGDLLGFLWTCRRDVTMDGLLYDLTEKQ
VYHIGKQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT
IPLKWLAPERLLLRPASIRADVWSFGILLYEMVTLGAPPYPEVPPTSILEHLQRRKIMKR
PSSCTHTMYSIMKSCWRWREADRPSPRELRLREAAIKTADDEAVLQVPELVVPELYAAV
AGIRVESLFYNYSML

SEQ ID NO: 236_AA098024_M

LQEKHLFHGDVAARNILIQSDLT PKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL
LRPASIRGDIWSFGILLYEMVTLGAPPYPEVPPTSILQYLQRKKIMKRPSSCSHAMYNIM
KCCWRWSEDSRPLLQQLQRLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF
SVL

SEQ ID NO: 237_SGK2ALPHA_H

MNSSPAGTPSPQPSRANGNINLGPSANPNQAQPTDFDFLKVIGKGNYGKVVLLAKRKSDGAF
YAVKVLQKKSIKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLDYVNGGE
LFFHLQRRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLDTDFGL
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVS
QMYENILHQPLQIPGGRTVAACDLLQSLHDKDQORQLGSKADFLEIKNHVFFSPINWDDL
YHKRLTPFPNPNVTGPADLKHFDPFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE
DDDILDC

FIGURE 1BB

SEQ ID NO: 238_CCRK_H

MDQYCILGRIGEGAHGIVFKAKHVETGEIIALKKVALRRLEDGFPNQALREIKALQEMED
NQYVVQLKAVFPHGGSFVLAFAEFMLSDLAEVVRHAQRPLAQAVKSYLQMLLKGVAFCHA
NNIVHRDLKPANLLISASGQLKIADFGLARVSPDGSRLYTHQVATRSVGCIMGELLNGS
PLFPGKNDIEQLCYVLRILGTPNPQVWPELTELDPYNKISFKEQVPMPLLEEVLPDVSPQA
LDLLGQFLLYPPHQRIAASKALLHQYFFTAPLPAHPSELPIPQRLGGPAPKAHPGPPPHIH
DFHVDRPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLPGFTLQGLPMA
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239_TESK2_H

MDRSKRNSIAGFPFRVERLEEFEGGGGEGNVSVQVGRVWPSSYRALISAFSRLTRLDDFT
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINS
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLIKRDENGYSAVVA
DFGLAEKIPDVSMGSEKLAVVGSFWMapeVLRDEPYNEKADVFSYGIILCEIIARIQAD
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLTFNCCNMDPKLRPSFVEIGKTLLEEILSRL
QEEQERDRKLQPTARGLLEKAPGVKRLSSLDDKIPHKSPCPRRTIWLRSQSDFSRKP
PRTVSVLDPYYRPRDGAARTPKVNPFSARQDLMGKIKFFDLPSKSVISLVFDLDAPGPG
TMPLADWQEPLAPPIRRWRSPLPGSPEFLHQEACPFVGREESLSDGPPRLSSLKYRVKEI
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEERPAGSTPATF
STSGIGLQTQKQDG

FIGURE 2A

SEQ ID NO: 1_X69117_H BARK2_H

ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC
AAGGCGACCCCGGCCGCCCGCCAGCAAGAGGATCGTCCTGCCGGAGCCCAGTATCCGG
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA
CCTCAGGTGAAGTTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC
CGCCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTTCTTTCCTGT
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA
GTGACATCAACTCTTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC
ATTTTTCAAAAATTTATGGAAGTGACAAGTTCCTAGATTTTGTGAGTGGAAAAACGTT
GAATTAAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA
GGATTCCGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA
ATCATGTTGTCTCTTGTGACACAGGAGACTGTCCTTTCATTGTATGTATGACCTATGCC
TTCCATACCCAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTTCAC
TACCACCTTTTCAACACCGGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA
ATCATTCTGGGTCTGGAACACGTGCACAATCGGTTTGTGTCTACAGAGATTTGAAGCCA
GCAAATATTCTCTTGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCTGC
GATTTTTTCAAAAAGAAGCCTCATGCGAGTGTGGCACCCATGGGTACATGGCTCCCGAG
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGCCGACTGGTTCTCCCTGGGCTGCATG
CTTTTCAAACTTCTGAGAGGTCACAGCCCTTTTCAAGACAACATAAAACCAAAGACAAGCAT
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACCTTCCAGACACCTTCTCTCCTGAA
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTCAC
GGAGGCGGCTCACAGGAAGTAAAAGAGCACAGCTTTTTTCAAAGGTGTTGACTGGCAGCAT
GTCTACTTACAAAAGTACCCACCACCCTTGATTCCCTCCCGGGGAGAAGTCAATGCTGCT
GATGCCTTTGATATTGGCTCATTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTCTCTCTGAACGCTGGCAGCAAGAA
GTAACGGAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT
ATGCACGGGTACATGCTGAAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT
TTTTACCTCTTTTCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAATGCAAT
TTGTTTCAAGATAAAAGGAGGGAACAATTTGTCTTGCAATGTGAGAGTGATCCAGAGTTT
GTGCAGTGGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCGT
GCCCCGAAGTTCCTCAACAAACCTCGGTCAAGTACTGTGGAGCTCCCAAAGCCATCCCTC
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2_AA144574_M BARK2_M

CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA
CGTGAGGATATCGGATCTCGGCCTTGCTGATTTCTCAAAAAGAAGCCTCATGCCAG
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA
CGTGACGCTTCCAGATGCCTTCTCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGGGCACGAGAGTTGAAGGAGCA
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTAACGGAAGTACCCGCCACCCCT
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACGCCGTCAA
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTACCTGTTCCCCAACAGACTGGAGTG
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTACTCAGGATAAAGGGAGGGAAGCAATT
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC
CTTCAATGAGGCCCAGAGACTGCTGCGCCGTGCCCCCAAATTCCTCAACAAACCACGGGC
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTACAGAAATAGCAGCGGCCTCTGAAC
CACAGAGCAGCGGGGCTGAAGGAGGGGCCCCAGCTCTTCAGCCCAGGAGTGGAACGAAG
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTCTTGAGCACTGACGGGGCTGCTCCA
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3_AA826850_H

GAAGAGGATGGGCTCGTCCATGTTCGGCGGCCACCGCGGGAGGCCGGTGTGTTGACGACAA
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CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCGGGGAGCTGGAGATCCT
GCAGGAGATCGAGCACGTCTTCCTGGTGAACCTCTGGTACTCCTTCAGGACGAGGAGGA
CATGTTTCATGGTTCGTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA
CGTGCACTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT
TGTCAACGGCGGGACCGGCTACTCCTTCAGAGTGGACTGGTGGTTCGGTGGGGGTGATGGC
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC
CCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGCTGTGGGACCACCTGAGCGAGAAGAG
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTCTGCACTGCGACCCACCTTTGAGCT
GGAGGAGATGATCCTGGAGTCCAGGCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAACAGAGAAAAGCTGAAGAGGAGCCA
GGACCTCCCGAGGGAGCCTCTCCCCGCCCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA
GGACGAGGCGGAACGCTCCGCCCTGCCCATGTGCGGCCCATTTGCCCTCGGCCGGGAG
CGGCTAGGCCGGGATGCCCCGTGGTCTCACCCCTTGAGCTGCTTTGGAGACTCGGCTGCC
AGAGGGAGGGCCATGGGCGGAGGCCTGGCATTACGTTCCCACCCAGCCTGGCTGGCGGT
GCCCCAGTGCCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCTGGGGCCCCGAGACCCGCCTA
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG
GGACAGGAGTCTTTGTCCCTGCTCAGCCCCGAGGCTGTGCACGGCCCTCGTCACAAGGTG
ACCCCTGCAGCACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCCTGGAGGTCAAGGGC
ATGGGTTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAAGTCTCCAGCA
ATTTCTGTATAGTTTTACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4_AA960957_H

GTCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG
GAATATGGGCGGGAACCACTCCCAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA
CTTTGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT
CGTGCAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG
CATCGAGAGGGATGAGGTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTTCATGGT
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTCAC
AGAGGGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA
TGTTACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG
CCCCGGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTCAACAT
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGAT
TCTAGAATCCAAGCCACTTCACAAAAAGAAAGCGATTGGCAAAGAACAGATCCAGGGA
TGGCACAAAGGACAGCTGCCCCGTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG
GGAGGAATTCATCATATTCAACAGAGAGAAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA
GCTCTTGACACCGACAGCCGAGGGGGAGGCCAGGCCCCAAAGCAAGCTCCAGGACGGGTG
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCACACTTG
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCTCTTTGTGC
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGA
GCTGGGAAGCCTGGGTTCTGGTCCCATCTCCATGACTGATTACGTGTGACCTCAGACAA
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTAAACACTTCTGCC
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT
TGATATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC
ATTCCCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA
GGGCACCTCCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCCCTT
CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT
CTGGCAGGCCACAGTCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCTCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCTCATTTAAGAAGACTATCCTTACCTTTT
AGTTTCAGCAGTCTCACACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA
TTCAGATGAGAGTTGGGTCGCTGAGCATTGGTTACTCCTGCAGAGTGTAATCAGCACCCC
ATCCAACCTGGCCCGAAAGCCCAGACCTGCAGCAGAACTCTCCAACCTCTCTATCAGCTTTC
AGGGTTTTCTCTCCTGGGAAGGGTGTAATAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG
AAAGTTTATTTTCAGGAGGAAAATGGGTTTACACAAAAAGCAAACACTACATTCTGATCTGCT
CAGGGAGAAGCTTGCCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT
TGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAACTAAGTGGGAGACCTT
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCTCATTTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG
GATGACTCATAGAATGGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTC
TTCCTTCACTCACCCAGCAGGTCAGTTTTCTGTGCAACAAACCTGTTTAGGATTCTTCC
AAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTGTTACATCCTGCTGAAGTTCGACTGTG
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ATTTTTATTTTTTAAAAAGAAATAGTCAGTGTTTTCTCCTTCAACCGAGACTATTTTC
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTTTTGCACACTTTTCTTTACTTCATGTCCC
CATCAACAACCGTCTCTGCTCCCCACCTCCCCAGGAAATAAGGGGCCTGCTCCTCTCCCT
ACTGTGACCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGA
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCCTGGTTCTGTTCAAGT
TGGCATTTCTTGTGTTGGAATAAACTATTTCTTGGACATTCTTC

FIGURE 2D

SEQ ID NO: 5_TBK1_H

TCCTGAGTCTCGAGGAGCCGCGGGAGCCCGCGGCGGTGGCGCGGCGGAGACCCGGCTG
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG
ATGTTCAAATGAGAGAATTTGAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTTGTC
CATGTGGGAGTTTATACACTGTTTTAGAAAGAACCTTCTAATGCCTATGGACTACCAGAAT
CTGAATTCCTTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCACTCTTT
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG
AAAAGTGTTGGGGTTTTGACCAGTTTTTGCAGAACTAGTGATATACTTCACCGAATGG
TAATTCATGTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTCATAGCTATA
ATACTGCTACTATATTTTCATGAAGTGGTATATAAAACAAACCAAATTTCTTCAAATC
AAGAAGTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT
TCCCTAAAAGTACTGAGGAAAACCTATATTTGTAGTAAGCCGGAACCTCTGAATACCA
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA
TTAAAGATGATTACAATGAACTGTTTCAAAAAAGACAGAAGTTGTGATCACATTGGATT
TCTGTATCAGAAACATTGAAAAAACTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC
TGGAAGCGGCAGAGTTAGGTGAAATTTAGACATACACACCAAATTTGTTGAGACTTTCCA
GTTCTCAGGGAACAATAGAAACAGTCTTTCAGGATATCGACAGCAGATTATCTCCAGGTG
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TGTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTTAAAAAGTATG
AGGCATTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT
TATTATCGCTGACTAATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAT
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AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGA
TGAAGAAATTAAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA
TTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT
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TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTGGCTGCTGTGAA
GATGTAATTTTATCTTTTAAACATTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC
TAAATAAGTTATTTCTCTGACCGCCTACTGGAAATATTTTTAAGTGAACCAAAATAGG
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAATGGTAGAACGGTGGCTAC
TGTGAGTGGGGAGCAGAACCGCACCACTGTTATACTGGGATAACAATTTTTTGAAGG
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCAGATCCCAGTTATCCTTGTATCCATG
TAATTTTCAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTAAGAACTATTC
ATTTTTTCTCTTGGCCATAAATGTGTAATTGTCAATTAAGGTCATTTCAACT

FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT
CAATTTTAAAAAA

SEQ ID NO: 6_AA305176_H

TGGCTGCTCGCGGAGGGGAGTGTACGCGGGGCCGCTGTAGGCTGTCCAGCGATGGATCC
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATTAGCCG
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA
TGCCTGGCACTAAGCAAAAGCCCATTCATTGTCCATTTGTATTATTCACTGCAGTCTGC
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCTTACA
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT
TATTTCTAATGAGGGTCATATTAACTGACGGATTTTGGCCTTTCAAAAGTTACTTTGAA
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA
TTATTCAAGAACCCAGGACAAGTGTATCGCTTATCAGCTCGTTGGGATTTAACACACC
AATTGCAGAAAAAATCAAGACCCTGCAACATCCTTTGAGCCTGTCTGTCTGAAACATC
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA
TTCTAGCAAAATTACTAAATCATGTCTTGAACAGTTGCCTCCAACCCAGGAATGCCTGT
GAAGTGTCTAATTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG
TAGTCAATCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAATG
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA
AATGAATGTGAGAAATATTATACCTTTTTCATATAAATTCATAAAGAAATGAAATTGTTA
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCCTGCACATTCTGTCAAATTC
TTTTGAAATATTTTCATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA
GATTCTTGCAGTAAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTTGGTTTTGTTTTATTTTGT
TTTTAACATATGTCATTTAAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7_AA116841_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG
CAATGGACATGCTTTTAAACCATTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAAC
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTTCG
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCAATTTTTATCTAATTTGTGA
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAAATTACTAAGTACAACAGTTTTTACAG
AATTAAAATACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAAGTGTATATAA
GCCATAATAGCTTTTTTTCATCTTATTTATTCACTGCACTTTATGAAGAGCAAAGTATCAA
TAAACTAAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8_AA256100_H

AGGGAGCTGACGGGCGCCCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC
GCGACCGGAGGAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC
TATGAGCAACCATAACCGGGAAAGAGTGAAGTGTAGCCAAGCTCACATTGGAGAATTTTAA
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATTAGAAGTGGC
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTGATCACAACACGCTCG
CAAAGAAACAGAGTTCTTACGGCTCAAAAGGACCAGACTTGGCTTGATGACTTTGAGTC
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA
GATGTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT
CTACATTTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTTCATCCATCG
GGATATTAAGCCAGACAACCTTTTATTGGATGCCAAGGGTCATGTAAAATTATCTGATTT
TGGTTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA
CAACCCACCAAGTGACTTCTCATTTTCAGAACATGAACTCAAAGAGGAAAGCAGAACTTG
GAAGAAGAACAGGAGACAACCTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC
AGAAGTATTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA
CAGAAAAGTGATGAACTGGAAAGAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA
GAAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAG
TGGAGTAGAAGAAATAAAGGTTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA
TGACTTCCCTGAATCTGATATTTTACAACCAGTGCCAAATACCACAGAACCGGACTACAA
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC
TGAAATACTCCTGAAGATGGTGGTGCTTATTGACTACAAGAGGAAATTCTACAGGATTAG
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAAATAT
TTTATTATTTTTGTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC
TTTCTAACTGCCTGCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT
TTGAACTGTAAACACCTCTAATCAATTCAGGAGAAACACATATCATTTAAAGCAACATAGG
CTAACCTGTAGGTAACACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA
ATCAGTAAAGCCATCTTCCATAGTTGGTGTGTAGAACATTGCCCTATTGGTTTGGACATC
TGTAAGATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAACTTCACAGTAAGGAG
TGACAAGTTTTATAATAAGGAAGACAAAGTTTAAACACCTTCACTCAAGCACTCCACTAATA
TATTTACGTTGCATTTCAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGAATTTCTT
TTTTTAAACAAGAGGACATGGCATTATTTTAAATTTGATTATGGTGAGTTGAATTTAAGACA
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTTTATTAACTATTTTTTTTAAATGTC
AACTTCTATCATGTAAATGGACTTATAGAGAACAAAAAGCTATTTACTTTGGTTTTCTA
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTTATTCTTTTGATGAAAATTTTTCCCTT
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAGATCTT
GAACAGAGTGGATGTTCACAACTGAGTAGAATTTTCTTTCTGTGGGCATGCTGTATTC
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAGGGCAATATTGTTCTTGTGTTAG
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTTGT
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATCTTTGGGTATCTCTAAGAATT
AAATAATCTTTCTAGCTTAATATTTTAATTCTAATCAAACAACCTCTGAGGTTTTGGTT
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAAATGGCCTAATGTTTGTACATAAC
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATATAAATGATCTATGA
TCAAATCTAAAGTGATGAATTATTTGTAGGAATGTCTTCCTAATGGGGAAGAATTGCAT
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG
TGTTTCATAAGGCCATCCTGTTTCCCCCACTCCCCATTTTTGGTTTGTCTTTCTTTTAA
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACCTCCATTTTCTAGTCTGGAT
TTTTTGAGTATTTAGGAAAGAGAGCTATTA AAAACTCTGGGGATTTCTCAATGTGACTAA
CTCTAATTTTTCTAATTATAACTGCCTTTAATTAACATAATATTAACCTTTTGCTGAGGTT
TATGAGATTTTCTACCCACATCGCTCCCTTTTTTTAAAGGACTGTTTTGCTAGTG
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCCTAGTTCTAGTATGGTAA

FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA
GAAACTGATTTACCTAAGTTTACTTTTTTAATTGCATAATAGAGCATTTTTTGTGTTTGAGT
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTTACTTTCTTGGCACTGGAAG
GGTAGTTCTGAAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAGCATTTCTTAAGTGCTATCTAAAAGC
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTCATGATGCAAATTAAGT
AGATAATTTGCAAAGTACCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTTC
AGGTGAATAATTTAATTTAAATGACAAAACCTATCTAGTCAACTGGGCATAATGACATT
TTCTTTAAATTAGACTCTATTTTGAATTTAAAGAGTTTTATTATAAACCGTGTGTTTTTG
TAGACTTTGACTTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTTGTGCTGTCT
GAAAATAAGGAATTGCTTATAAACAGCCACTTCTGAATACAATATGTAGCTGATTTAAT
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GCCTAAGATAGGGTTTTCAATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT
TTTATGTAAATCTCTAAATTTAAATATTTTAAAGTACATTTATTTTTGGTGTTTTATTGT
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TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA
ACACATTCTCCTTTGAATTGTTAAAATTCAGAACATTCAAATAACTGTTTTGCTACAAC
CCATGATTATTTTCCCTGTTGTGTTATTTAAATTTACTTTCTCTTTAGAAGTGCACTTAT
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA
CTACTAGAGATATTTTAGATTTTATGAAAAAATGTGAGGGGATATTGCTGCTTTAAAA
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTGAGCAAT
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTGAGTTACTGAGTTTCAAAAA
TGTTTTGGTGGCATGAGGACAAAATTTTATTGAAGGTAAGATAAGAATAAAAACTATGTT
TAC

SEQ ID NO: 9_AA210825_H

CACGAGGGCTACTGGCGCCTGGCGACCCTCCCTGCCCCCACCCAACCCCGCTCCGGCAA
CGCCCCCTTCCTCACGGCTCCCGACCGAACTTTTCTCCAATTCTGCGACTCGTGAGATT
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCCTGGCCGGTCCGGTCCC
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA
CCCCCAAGGACCCCGCCATCCTCAGGTCCCCTCCGCCTGCCAGATCTTTTCTCGGATCCC
CGCTCTCCCAACCTGCTCACGAGATCCCGCGGATCTAGAACCAGGGTCCCCCGGGC
CCCCCGGCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCCTCCCCCATGGCCAC
CGCCCCCTCATATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGGTCTCCTCCGCCCC
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCCGGGT
CCGGGGTCTCCTTTACATCCAGATCGGGCTGACCCGCGAGTTCGTGCTGTTGCCCGCCG
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGGACCAGAAGTTCCTG
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCACGTCGG
CCAACCTCCTGCAGCTGGTGCCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG
TGGTGTGTCGGCCTCGGCCACCTTCGAGGACTTCAGATCCGCCCCGACGCCCTCACGG
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG
TGCGCCAGGGCCTCAAGTGCATGGCTGCGGGCTGAACTACCACAAGCGCTGTGCCTTCA
GCATCCCCAACAACTGTAGTGGGGCCCCGAAACGGCGCCTGTTCATCCACGTCTCTGGCCA
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA
GCCGTAGCACCACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCTCCTCTCTG
CCTCATCGTATACGGGCCGCCCCATTGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG
TGCCGCACACCTTCTCATCCACAGCTATACACGGCCCACCGTTTGCCAGGCTTGCAAGA
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGTT
GGGTGGTTTATTACAGCAACAAGGACACGCTGAGAAAAGCGGCACTATTGGCGCCTGGACT
GCAAGTGTATCAGCTCTTCCAGAAACAACGACCAACAGATACTATAAGGAAATTCCGC
TGTCAGAAATCCTCAGGTGGAGTCCGCCAGAACTTCAGCCTTGTGCCGCCGGGCACCA
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG
GCGGGACTCCGGGTGGGCCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA
CAGCCATCCGCCAGGCCCTGATGCCCGTCACTCTTTCAGGACGCACCCAGCGCCCCAGGCC
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT
TTGGAGTGGTCTATGGAGGAAAAACCCGGAAGACAGGCCGGGACGTGGCAGTTAAGGTCA
TTGACAAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGATGTTTCGAGACGCCTGAGA
AAGTGTGTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG
AGAAGGGCCGGCTGCCTGAGCGCCTCACCAAGTTCTCATCACCAGATCCTGGTGGCTT
TGAGACACCTTCACCTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC
TGGCATCAGCAGACCCATTTCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA
TCGGCGAGAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGGCGTGATCATGT
ACGTGAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC
AGAACGCCGCCTTCATGTACCCGGCCAGCCCCTGGAGCCACATCTCAGCTGGAGCCATTG
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA
AGATGGGAGAGCGATACATCAGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCACGGACAGGGATCTCGGTGGGGCCTGTC
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTTCTCTGAGGTCTTG
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTCACAGGATCCCAGCAATGAACTG
TTCTAGGGAAAGTGGCTTCTGCCCCAACTGGATGGGACACGTGGGGAGTGGGGTGGGGG
GAGCTATTTCCAAGGCCCTCCCTGTTTCCCAGCAATTAAAACGGACTCATCTCTGGCC
CCATGGCCTTGATCTCAGCAAAA

SEQ ID NO: 10_AA127299_H

ATTCAATTCATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT
GATCCTTACATCAAAATCACAAATCTTCTCAAAAAACGAAAGTGATTAAGAAAACCTTG
ACTCCAACCTTGAATGAACTTTTTTTGTGCATTTTCCAGAAAAACAACCTTGAATTA
GAATGTTGGGACCACGATACTTTTTCAGATGATTTTATTGGCAAGGCTTCCATTTCTTTG
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAAGGA
GAATTTGCAGGAAAA

SEQ ID NO: 11_AA316804_H

ATGTCTGCAAATAATTCCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCCT
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCCTAAGACGGGACTCTTGCCCGACTC
TCTAATGGAAGCTTCAGTGCACCATCACTACCAACTCCAGAGGCTCAGTGCATACAGTT
TCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAACTG
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT
GGATTCTTTGGCATGTATGACAAAATCTTCTCTTTCGCCATGACATGAACTCAGAAAAC
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGTT

FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTCTGTCCACATACTCTCTATGTACAT
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT
CCAAATAACTGTAGTGGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA
CATGTCCACCAGGAACCAAGTAAGAGAATTCCTTCTTGGAGTGGTCGCCCCAATCTGGATG
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCACACACATTTGCTGTTCACTCTTACACC
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG
CAGTGTAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAGTACCAAGAGAC
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCCTCCAGTCTGGGAACAGATACAGATATA
CCAATGGATATTGACAATAATGACATAAAATAGTGATAGTAGTCGGGGTTTGGATGACACA
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG
GAAAAGAGATGAAGAAGCCGT'AAAAACAATCAGTCCATCAACAAGCAATAATATTCGCTA
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAATGGTGAAGGAA
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAAGAGGCATTATTGGAGACTT
GACAGCAAATGTCTAACATTATTTTCAAGATGAATCTGGATCAAAGTATTATAAGGAAATT
CCACTTTTCAAGAAATCTCCGCATATCTTACCACGAGATTTACACAAACATTTACACAAGGC
AGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATACCTCGTTGGTGAGAAC
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA
CAGAGCTGGGAAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT
TGCACTTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT
AATTGTCAGATTCAAGGAGAATGTGGATATCAGTACTGTTTACCAGATCTTTGCAGATGAG
GTGCTTGGTTTCAAGCCAGTTTGGCATCGTTTATGGAGGAAAAACATAGAAAGACTGGGAGG
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT
ATGTTTGAACCCCAAGACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC
ACACAGATACTTGTGCTTTGAGGAATCTGCATTTTAAGAATATTGTGCACTGTGATTTA
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCTCAGGTGAAGCTGTGTGAC
TTTGGATTTGCACGCATCATTGGTGAAAAGTCATTCAAGGAGATCTGTGGTAGGAACCTCCA
GCATACTTAGCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCTTTTAAATGAGGATGAA
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA
ATTTCTGGTGAAGCAATTGATCTGATAAACCAATCTGCTTCAAGTGAAGATGAGAAAACGT
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC
CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGATGCT
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CCTAATCCAGATGATATGGAAGAAGATCCTTAA

SEQ ID NO: 12_PKNBETA_H

ATGGAGGAGGGGGCGCCGCGGCGAGCCTGGGCGGAGCCAGTGGCCCCAGAGGATGAGAAG
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CGGCGCGTGGCCACAGACCGCGCCACTTGGGCCATGTGCAGCAGCTGCTGCGTCTCTCC
AACCGCCGCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCCGAATCCTGCTG
CCCCGCCCTGGGCTTGGCCAGCTGAGCCTGTGGCCTCAGGACCCCGGCGCTGGGCAGAG
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCEAAGGAGAGGAAG
CTCCTTGACAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGGAGCCAGGGCCTGAGCTACTGGCG
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAACGTG

FIGURE 2J

GTGAAACTGCTTAGTAGCCGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCAGGQC
CAGCTACAGGAGTCTCTCAGAACTGGACCTCTGCGCCTGGCCTTGGAGCAGCTGCTG
GAGCAACTGCCTCCTGCCCACCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCACCGCCCTAACAGGGACA
CTGCAGGTCCGCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA
GCGGCCGCACTGGCCAGCAGCCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT
GTGGGGCAGACGGGCTGGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTCATC
CCACTGGAGCGAGCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA
TGTGGCGTGGCCTTCTGAGACTTGAAGACTTCTGGACAATGCCTGTACCAACTGTCC
CTCAGCCTGGTACCGCAGGGACTGCTTTTTGCCCAGGTGACCTTCTGCGATCCTGTCAAT
GAGAGGCGGCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC
TTCCTGAGGCGTTTCGCAGATGAACCTCGGCATGGCGGCCTGGGGGCGCCTCGTCATGAAC
CTGCTGCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCTAAAGGATGCCCTCGGACC
CCAACAACACTGCGAGAGGCCTCTGACCTGCCACTCCCAGTAATTTCTGCCCCAAGAAG
ACCCCTTGGGTGAAGAGATGACACCCCCACCCAAGCCCCCACGCCTCTACCTCCCCCAG
GAGCCAACATCCGAGGAGACTCCGCGCACCAAAACGTCCCCATATGGAGCCTAGGACTCGA
CGTGGGCCATCTCCACCAGCCTCCCCACCAGGAAACCCCTCGGCTTCAGGACTTCCGC
TGCTTAGCTGTGCTGGGCCGGGACACTTTGGGAAGGTCCTCCTGGTCCAGTTCAAGGGG
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCCT
TTCCTGCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCGCTTTGTGACTGAG
TTTGTGCTGGTGGTGACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG
GCCCGCTTCTACGTGGCTTGTGTTGTCTGGGGCTGCAGTTCTTACACGAGAAGAAGATC
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GCAGACTTTGGACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT
GGCACCCCGGAGTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACAGGCCGCTC
GACTGGTGGGCGCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA
GGGGACACAGAGGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCGGC
TTTCTGTGCGTGCAAGGGCTTGAGTTCAATCAGAAGCTCCTCCAGAAGTGCCCGGAGAAG
CGCCTCGGGGCAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC
ACCAACTGGCAAGCCCTGCTCGCCCGCACCATCCAGCCCCCTTCGTGCCTACCCTGTGT
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACC
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TTTGTGTCAGAGCGATTCTTGAACCTGA

SEQ ID NO: 13_AI021023_M PKNBETA_M

GCTGAAGTGGGATAACCTTCTGCTGGATGCCCAGGGATTCTTGAAGATCGCAGACTTTGG
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GTTCTTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACACGGGCTGTGGACTGGTGGGG
GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA
GGAAGAGGTGTTTGACTGCATCGTCAACATGGACGCCCCCTACCCGGCTTTCTGTGCGGT
GCAAGGGCTTGAGTTCAATCAGAAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGGC
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA
AGCCCTGCTCGCCCGCACCATCCAGCCCCCTTTGTGCCTACCCTGTGTGGCCCTGCGGA
CCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACCCACCTGCACC
CCACAGCCTCCTCACTGCCCCCAACAGGCCGCCTTCCGGGACTTCGACTTTGTGTGTCAGA
GCGATTCTTGAACCTGAGGGCATCTCCTGGCACCTCTGTCCCCTTCCCCACAGACTG
TTAGAGCCTCTGCTCGTTACCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA
GACCTGGCCCAGAAAGGGTGCCGCAGCAAGGAGTGATATGGTTTGTCTTTTAAAGACTGG
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14_H19102_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA
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GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGGCCAGTGCCT
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG
CTGAAGATTTTAGGCCTCGTGGCTAAAGGCTCCTTTGGAAGTGTCTCAAGGTGCTAGAT
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCAAGGTAAAGGTCTACAGAGG
GATACCGTGAGGCAGTGCAAAGAGGAGGTTAGCATCCAGCGACAGATCAACCATCCCTTT
GTACACAGCTTGGGGGACAGCTGGCAGGGAAAACGGCACCTTTTCATTATGTGTAGCTAC
TGCAGCACAGATCTGTACTCCCTTTGGTTCGGCTGTTGGCTGCTTTCTGAGGCTTCCATC
CGTCTCTTTGCTGCCGAGTTGGTGTGGTACTGTGTTATCTCCATGACTTGGGCATCATG
CATCGAGATGTGAAGATGGAGAATATTCTTCTAGATGAACGAGGCCATCTGAAACTGACA
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT
CTTCAGTACATGGCCCCAGAGGTCCTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG
TGGTCCCTGGGTGTCTTGCTTTTCTCTGCGGACTGGAAAGTTTCCAGTGGCTGCAGAG
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGAAGTCTGAGATCCAGCTTCT
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCTCCATCGT
CTACGTTATCTGCATCACTCCAGGTCCACCCTTTCTTTTCGGGGTGTGGCCTTCGACCCA
GAGCTCCTACAGAAGCAGCCAGTGAACCTTTGTACGGAGACACAAGCTACCCAGCCCAGT
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC
CCTATCCCTGCTTGA

SEQ ID NO: 15_AA476563_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAAGTCTTGGGACTTGACTTT
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GGAGACAGTGCTTCTAGGAGTTTAAATACTAGTGAAAGCAAGGTAGAGTTTAAAGCTCAG
GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTTCGTTTAAAGATGCTGCT
TTTGATGATGTGAGTGGTACTGATGAAGGAAGACCTGATCTTCTGTAAATTTACCTGGT
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAACTAAT
ATAGGGATAATAGAAAATAAATCTTGGAAAGCCCTGATGTTTTATGCCTCAGGCTTAGT
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAACTGAGTGATCCCTCTGGG
CCCAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT
GTAGCAGCTGTTGATCATAGTAGTTTACAGGAGATATGCTTTTGTACCCAGCTCAGATCCT
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAGCAGTAACTGCAACAACACAGAAGAAAGC
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CCAATTCTTTATTCCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA
GGAGACAAGGAAATACATCAGATTTTTGAGGACCTTGATAAAAAATTAGCACTAGCCCTCC
AGGTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT
GATGCTTTACATAGAGAGGGAATTGTGTGCCGCGATTTGAACCCAAACAACATCTTATTG
AATGATAGAGGACACATTACAGCTAACGTATTTAGCAGGTGGAGTGAGGTTGAAGATTCC
TGTGACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTTGGAGCAATCACTGAA
GAAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCTCTTTGAACTTCTCACTGGC
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAGTTCAATCCTCTG

FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTGAAGATATCAAATCTCATCCATTTTTTTACC
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16_AA626690_H

ATGCTACCATTCGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTTCAGCGGC
GGCGGCGCGAGCAGCGGCGAGGTAAATGGTCTTAAAATGGTTGATGAGCCAATGGAAGAG
GGAGAAGCAGATTCTTGTTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT
CAGGGGTCAATTTGGAAAGGTTTTCTTGTAGAAAGAAGACCGGTCTGATGCTGGGCAG
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTAAAAGTTTCGAGACAGAGTTTCGGACA
AAGATGGAGAGGGATATACTGGTGGAAAGTAAATCATCCATTTATTGTCAAATTGCACTAT
GCCTTTTCAGACTGAAGGGAACTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATTCTACCTCGCA
GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGAATCAGC
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT
GTTCTTATGTTTGAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG
ACCATGAATATGATATTAAGCAAACTTGAATGCCTCAATTTCTTAGTGCTGAAGCA
CAAAGTCTTCTAAGGATGTTATTCAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA
GTTGAAGAAATCAAAGACATCTGTTTTTTGCAAATATTGACTGGGATAAATTATATAAA
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGAAAACCAGATGATACTTTTTGTTTT
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAAT
GCTCATCAGCTCTTCAAAGGATTCAGCTTTGTTGCAACTTCTATTGCAGAAGAATATAAA
ATCACTCCTATCACAAGTGCAAAATGTATTACCAATTGTTTCAGATAAATGGAAATGCTGCA
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGGCTCCTACTCTGTTTGC
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAAATGTTTCTCGGAACGGGAGGCT
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CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGAGATTCA
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAAATGGACTTCTCTTA
ACTCCATGCTACACTGCAAACTTTGTTGCACCTGAGGTTCTTATGCAACAGGGATATGAT
GCTGCTTGTGATATCTGGAGTTTAGGAGTCCTTTTTTACACAATGTTGGCTGGCTACACT
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA
AAATTCTCTTTGAGTGGTGGAACTGGGACAATATTTTCAGACGGAGCAAAGGATTTGCTT
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCAGCGACGGAGCATGAAAAAGCGA
ACATCAACTGGCCTGTAA

SEQ ID NO: 17_AA215680_H

ATGAGCCTGGTGGCCTGTGAGTGCCTGCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTGCAACAGGGTGGCTCTGGGA
GTGCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC
CTGGAGCGGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG
GACGTGCTGCTCCGTGGCATAACGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG
CTGAAAATTACCAAATACCTGCGGCGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGCGGGTTTCAGCAGCCTGAGGCTCCGGCCCCATT
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTCATCGAG
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC
AGGTGCCACATGGTGAGCAGGGAGCGGCTGACCATCATCCACACGGAGTCCCCTACATG
ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCCTGCACCTGGAGCATGTG
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG
ACCCACAGCGAGGCTTCCCTCAGGCCATGCCCCTGGCCAGGACAGAATCGCCCTGGAGCCT
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACCAGACCCAGAGG
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG
GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAATCAGACGCTGGG
CCCCCTCGGGGGCTCACTTGGGTTCTGAGGGGGCGGCGCCGGTGCTAGGGGGCTGTGGC
CGAGGCATGGATCAGAGCTGCCTGTGAGCAGATGGGGCGGCGGGGGCTGTGGCAGGGCC
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG
GAGGCGCTGCACGAGCAGGGGGTGTGTGCCGGGACCTCCACCCCGGGAACCTGCTCCTG
GACCAGGCAGGTACATCCGGCTCACATATTTTGGCCAGTGGTCAGAGGTGGAGCCCCAG
TGCTGCGGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA
ATGGCACTGTCCAGAGCCACCTTTCAGGAATCCAGGCCACACCCAGCTCCAGCTGCCC
GAGTGGCTCAGTCGCCCAGCGCCTCTCTGCTGACTGAGCTGCTGCAGTTCGAGCCTACC
CGGCGCCTGGGCATGGGAGAAGGTGGTGTGAGCAAACTCAAGTCCCATCCCTTTTTTCAGT
ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18 SGK_H

ATGACGGTGAAAACCTGAGGCTGCTAAGGGCACCCCTCACTTACTCCAGGATGAGGGGCATG
GTGGCAATTCTCATCGCTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAG
AAGATTGCCAATAACTCCTATGCATGCAAAACACCCTGAAGTTCAGTCCATCTTGAAGATC
TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCTTCTCCTCCACCAAGTCCTTCT
CAGCAAATCAACCTTGGCCCGTCTGCTCAATCCTCATGCTAAACCATCTGACTTTCACCTC
TTGAAAGTGATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGCAGAA
GAAGTGTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG
AAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTTCCTGGTG
GGCCTTCACTTCTCTTCCAGACTGCTGACAAATTGTACTTTGTCTAGACTACATTAAT
GGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCAACGGGCTCGT
TTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTTAT
AGAGACTTAAAACCAGAGAATATTTTGCTAGATTCAAGGGACACATTGTCCTTACTGAT
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAAACATCCACCTTCTGTGGCAGC
CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGG
TGGTGCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCCTTTTATAGCCGA
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT
ACAAATTCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTCTCTTAATTAAGTGG
GATGATCTCATTAAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCCAAC
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCCATTGGCAAG
TCCCTTGACAGCGTCTCTGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCCTAGGC
TTTTCTATGCGCCTCCACGGACTCTTCTCTCTGA

SEQ ID NO: 19 AA107515_M

CGGGTCGACCCACGCGTCCGCCGGTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCCCTTACCTACTCCA

FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCTGA
ACGATTTTATTTCAGAAGATTGCCAGCAACACCTATGCATGCAAACACGCTGAAGTTCAGT
CCATTTTGAAAATGTCCCATCCTCAGGAGCCGGAGCTTATGAACGCTAACCCCTCTCCTC
CGCCAAGTCCCTCTCAACAAATCAACCTGGGTCCGTCCTCCAACCCTCACGCCAAACCCT
CCGACTTTCACTTCTTGAAAGTGATCGGAAAGGGCAGTTTTGGAAAGGTTCTTCTGGCTA
GGCACAAGGCAGAAGAAGTATTCTATGCAGTCAAAGTTTTACAGAAGAAAGCCATCCTGA
AGAAGAAAGAGGAGAAGCATATTATGTCAGAGCGGAATGTTCTGTTGAAGAATGTGAAGC
ACCCTTTCTGGTGGGCCTTCACTTCTCATTCCAGACCGCTGACAAGCTCTACTTTGTCC
TGGACTACATTAATGGTGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCTGG
AACCACGGGCTCGATTCTACGCAGCTGAAATAGCCAGTGCCCTGGGCTATCTGCACTCCC
TAAACATCGTTTATAGAGACTTAAACCTGAGAATATTCTCCTAGACTCCCAGGGGCACA
TCGTCTCCTCACTGACNTATTTAGCTGCGTAGAATCGAGCATAACGGGACAACATCTACCT
TCTGTGGCAGCGCTGAGTATCTGGCTCCTGAGGTCTCCATAAGCAGCCGTATGACCGGA
CGGTGGACTGGTGGTGTCTTGGGGCTGTCTGTATGAGATGCTCTACGGCCTGCCCCGT
TTTATAGCCGGAACACGGCTGAGATGTACGACAATATTCTGAACAAGCCTCTCCAGTTGA
AACCAAATATTACAACTCGGCAAGGCACCTCCTGGAAGGCCTCCTGCAGAAGGACCGGA
CCAAGAGGCTGGGTGCCAAGGATGACTTTATGGAGATTAAGAGTCATATTTTCTTCTCTT
TAATTAACCTGGGATGATCTCATCAATAAGAAGATTACACCCCATTTAACCCAAATGTGA
GTGGGCCAGTGACCTTCGGCACTTCGATCCCGAGTTTACCGAGGAGCCGGTCCCCAGCT
CCATCGGCAGGTCCCCTGACAGCATCCTTGTACCGCCAGTGTGAAGGAAGCAGCAGAAG
CCTTCCTCGGCTTCTCCTATGCACCTCCTGTGGATTCTTCTCTGAGTGCTCCCGGGAT
GGTTCTGAAGGACTTCTCAGCGTTTCTTAAAGTGTTTTCGTTAGCCTTTGGTGGAGTTG
CCAGCTGACAGAACATTTTAAAAGAATTTGCACACCTGGAAGCTTGGCAGTCTCGCCTGC
CCGGCGTGGCGCGACGCAGCGCGCGCTGCTTGATGGGAGCTTCCGAAGAGCACACCCTC
CTCTCAATGAGCTTGTGAGGTCTTCTTTTCTTCTCTTCTTCCAACGTGGTGCTAGCTCC
AGGCGAGCGAGCGTGAGAGTGCCGCTGAGACAGACACCTTGGTCTCAGTTAGAAGGAAG
ATGCAGGTCTAAGAGGAATCCCCGAGGTCTGTCTGAGCTGTGATCAAGAATATTCTGCA
ATGTGCCCTTTTCTGAGATCGTGTTAGCTCCAAAGCTTTTCTTATCGCAGAGTGTTCACT
TTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT
GTGGCGTGAGTGCTATGCCTGATCACAGACGGTTTTGTGTTGAGCATCAATGTGACAC
TTGCAGGACACTACAATGTGGGACATTGTTGTTTCTTCCACATTTGGAAGATAAATTTA
TGTGTAGACTGTTTTGTAAAGATATAGTTAATAACTAAAACCTATTGAAACGGTCTTGCAA
TGACGAGCATTAGATGCTTAAGGAAAGCATTGCTGCTACAAATATTTCTATTTTTAGAA
AGGGTTTTATGGACCAATGCCCCAGTTGTGAGTCAAAGCCGTTGGTGTGTTTCACTGTTT
AAAATGTCACCTATAAAACGGGCATTATTTATGTTTTTTTTTCCCTTTGTTTCAATTTCTT
TGCAATCCTGATTATTGTATGATCGTGTAAGGAAGTCTGTACATTGGGTTATAACACT
AGATATTTAACTTACAGGCTTATTTGTAAACCATCATTTTAATGTACTGTAATTAACAT
GGGTATAATATGTACAATTCCTCCTCCTTACCACACAACCTTTTTTTGTGTGCGATAAAC
CAATTTTGGTTTGCAATAAAATCTTGAAACT

SEQ ID NO: 20_AA109508_M

CCACCTGCAGCGGGAGCGCCGGTTCCTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGT
GGCCAGCGCCATTGGCTACCTGCACTCCCTCAACATCATTTACAGGGATCTGAAACCAGA
GAACATTCTCTTGACTGCCAGGGACACGTGGTGCTGACGGATTTTGGCCTCTGCAAGGA
AGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACCCCTGAGTACTTGGCACC
TGAAGTGCTTCGGAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGCTTGGGGCAGT
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCCAGATGTA
TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGACAGTGCCGCTGTGA
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCCGCTGGGCTCCAAAGCAGACTT
TCTTGAGATTAAGAACCATGTATTCTTACGCCCCATAAACTGGGATGACCTGTACCACAA

FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTGA
CCCAGAGTTTCAACCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC
CAGCAGCTCTGGGGCCTCAAGTGCATTCTGGGATTTTCTTATGCGCCAGAGGATGATGA
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAACTACTGAGGCCAGCTGGTATTAGTA
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAATAACAATGGCTTCAACGAGAAG
CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT
CCAATGTTAGGTTTGCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAG
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAA
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTC
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG
CCTCCTGGTGTGTTGGATTTTGATCTCAATGTGTAAATGACAGAGATGTAACAAGCTCAT
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21_AA887783_H

CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT
ACAAGGAAAGCTGCCCAAGTGTAAGNATTTCCAGCTCCGATGAACACAGAGAGAAAAAGA
AGAGGTTTACTGTTTATAAAGTTCTGGTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAACAGTTTCTGCTANGG
CCCTGAAGATTCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAAC
AAAGACGAGCAGGACTAAACGAATTCATTTCAGAACCTAGTTAGGTATCCAGAACTTTATA
ACCATCCAGATGTCAGAGCATTCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCAT
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAACATCAACC
TGGGACCGTCTGGAAATCCTCATGCCAAACCACTGACTTTGATTTCTTAAAAGTTATTG
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAACCGGAACTGGATGGAAAATTTTATG
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAGAGCAAAAACATATTATGG
CTGAACGTAATGTGCTCTTGAAAAATGTGAAACATCCGTTTTTGGTTGGATTGCATTATT
CCTTCCAAACAACTGAAAAGCTTTATTTTGTCTGGATTTTGTAAATGGAGGGGAGGGAC
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA
CCACATTTTGTGGGACACCAGAGTATCTTGACCTGAAGTAATTAGAAAACAGCCCTATG
ACAATACTGTAGATTGGTGGTGCCTTGGGGCTGTTCTGTATGAAATGCTGTATGGATTGC
CTCCTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG
ACAGGCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAATCATCTTTTTT
TTGAATCACTCAGCTGGGCTGACCTTGTAACAAAAGAAGATTCCACCACCATTTAATCCTA
ATGTGGCTGGACCAGATGATATCAGAAACTTTGACACAGCATTACAGAAGAAACAGTTC
CATATTCTGTGTGTATCTTCTGACTATTCTATAGTGAATGCCAGTGATTGGAGGCAG
ATGATGCATTTCGTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTTGTGAGCAG
TTTGCCATTTCAGAAACCATTGAGCAAAATAAGTCTATAGATGGGACTGAAACTTCTATTT
GTGTGAATATATTCAAATATGTATACTAGTGCCTCATTTTTATATGTAATGATGAAAAC
TATGAAAAAATGTATTTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT
TGATTAAATTTATATTCTTGTTAATAAGCTTATTTTTAAACAATTTAAAGCTATTAT
TCTTAGCATTAACCTATTTTTTAAAGAAACCTTTTTTGCTATTGACTGTTTTTCCCTCTA
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTAAACAGTCAATTTTCAGTTCAGCT
AACATATATTAATACCTTTGTAACCTTTGCTATGGCTTTTGTATCACACCAAAACTAT
GCAATTGGTACATGGTTGTTTAAAGAAGAAACCGTATTTTTCCATGATAAATCACTGTTTG
AAATATTTGGTTCATGGTATGATCGAAATGTAAAGCATAATTAACACATTGGCTGCTAG
TTAACAATTGGAATAACTTTATCTGCAGATCATTTAAGAAGTAACAGGCCGGGCGGGT
GGCTCACGCCTGTAATCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCA

FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT
TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA
ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG
CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22_R47805_H

ATGGCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA
CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT
GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGCTGCTGCCACTG
CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGC
TTCGAATGGCTCTTCTCGCCTGGTGCCTGATAACTCCCCCGTGC GGCTGAAGATGCTG
TACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCCACATCAAGGATGAG
CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGCTGGGTACCAGAAACACCTGTCGTCC
TGTGCGGCACCTGCCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC
GAGGTGAAGACAGAGATCAGTGTGGAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTC
CCCCTGCAGCCTGAGGCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC
ATCCAGATGAAGCTGGACCTAGAGCGGGAACCATTTAGAGCTGGTGACACAGAGCCCACG
GATGTGGCCCAGCTGCCCTCCCGGGTGCCCCGAGATGCTGCCCGCTACCACTTCTTCCTC
TACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTTCATCTACTCCATGCCG
GGGTACAAGTGACGATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTC
GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG
GCAGAGCTGACGGCAGAGTTCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG
CAGGCCTTCGCCAAGCCCAAGGGCCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCGC
GGCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23_H60215_H

CCACGCGTCCGGCGCCGCGAGCCATGGAGGGAGGCGGCGGGCGGGCGGGCGGGCTCGGG
TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCCTCCAGCCCGGCCCGGCCCCC
CGGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA
CCACCCGGCGAAGTGACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTTACAGC
ACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG
CACCAGGTCTGAATTCCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT
GACCACAGACCCATTCCAGGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA
TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCA
GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTCA
TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAGTGCAGTGTTTGGCGAGGA
AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC
AAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTCAC
TGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACC
GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC
GCATCTGCCTCGTCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC
TCATCAACCTGCAGCACTACGTCATCAAGGAGAAGAGGCTCAGCGAGAGGGGAGACTGTGG
TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGCACA
GAGACCTGAAGCTGGGGAACATGGTGCTCAACAAGAGGACACATCGGATAACCATCACCA
ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA
GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCGCGCGTACCGTGGCAAGCCCAGTG
ACATGTGGGCCCTGGGCGTGGTCTCTTACCATGCTGTATGGCCAGTTCCCCTTCTACG
ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCTGAGG
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGGACCCCC
AGCAGCGCCTGGCCGCGCCGACGTCCTGGAGGCCCTCAGTGCCATCATTGCATCATGGC

FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCAGTACGAGTTTG
AGA ACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC
GGAGCTGGGTACCCAAGCGGCAGTTCGGCAGCGCACCACCGGTGCGACGGCTGGGCCACG
ACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG
TGGCTGTCAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC
AGGGACAGGGACAGCCAGGTCAACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT
TGGGATGATTGCTCGATTGTTTGGTTTTTAAATCTGAGAAGCCTAGATAACTAATCTGCT
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC
AAGAGGGAGGAGGGAGCCTGCTCACCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTG
ACCTGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGACAGCTCGCTGCAGGCCCC
AGAGCGAGCTTCCCTCCTCCTGCTCTCCAGGCCCCCTGCCACAGCCTCTTTCGTCCTC
TCTCTTTCTGATCCAGGCCCCCTCAGTCCAAGCTTTGGAAAACCTTCACCTCATCTTAAAC
CAA ACTCAAATATATTTATTTTATTTTACCAT

SEQ ID NO: 24_SGK324_H

GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAGG
CCGCGGCCCGGGTTCGCGGAGAGGGGCCCCCAGCTCCTCCGGGGGCAGCAGCAGCTCGGGC
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC
ACGCGGACCCCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG
AACGGGGACCGCTACTTCAAGGGCCTGGTGTGTTGCCATCTCCAGCGACCGCTTCCGGTCC
TTCGATGCGCTCCTCATAGAGCTCACCCGCTCCCTGTCCGACAACGTGAACCTGCCCCAG
GGTGTCCGCACTATCTACACCATCGACGGCAGCCGGAAGGTACCAGCCTGGACGAGCTG
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTTCGTAAAGTCGATTACACC
AAAAATATTAATCCAAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT
GCTGCCTCCTCTGTGAAAAGTGAAGTAAAAGAAAAGTAAAGATTTTCATCAAACCCAAAGTTA
GTGACTGTGATTGCAAGTGGAGTGAAGCCTAGAAAAGCCGTGCGGATCCTTCTGAATAAA
AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC
TCAGGAGTCGTCAAGAGGCTCTGCACCCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG
CATCTGCCAGACTTTTTTTGGTGTATGACGATGTTTTTTATTGCATGTGGACCAGAAAAATTT
CGTTATGCCCAAGATGACTTTGTCTGGATCATAGTGAATGTCGTGTCTGAAAGTCATCT
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC
CGTTGCATAAGTCCTGAAGGTGTGAATGGAAAACAGATGCTCTGAATCATCAACTCTTCTT
GAGAAATACAAAATTGGAAAGGTCAATTGGTGTATGGCAATTTTGCAGTAGTCAAAGAGTGT
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT
ATCATTATGCTGGTCGAGGAGATGGAAACAGCAACTGAGCTCTTTCTGGTGTATGGAATTG
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTCGACCAAGTACACTGAGAGAGAT
GGCAGTGCCATGGTGTACAACCTTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG
TCTTTGAAACTGGGAGACTTTGGGCTTGGGACTGTGGTAGAAGGCCCTTTATACACAGTC
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTCTGTGGATTCCCACCATTC
CGAAGTGAGAACAATCTCCAGGAAGATCTCTTCGACCAGATCTTGGCTGGGAAGCTGGAG
TTTCCGGCCCCCTACTGGGATAACATCACGGACTCTGCCAAGGAATTAATCAGTCAAATG
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG
TCAGATGATGCCTCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAACAG
CACTTTAATAATGCGCTCCCCAAACAGAACAGCACTACCACCGGGGTCTCCGTCTCATG

FIGURE 2R

GTGAGTGGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCTTCCGTAGTCCTATTTTCATATGA
AGATTGGCTTGGCATGTGGAGGGCACTCATTCCGGCAACTCCCAGGCTTTGGGCACTGTGT
GGAGGGGCTTGTGTAGGGACCAGCAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC
CTGGCTGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACCTCCCTGCCTACCCCAAGGCC
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA
AAGCTAAACATATTTTCAGTTTTTAAAAAATCAGTGTTTTATAAAACACAGTTTGGGGCTTT
TAAAGGTACATAATCAAGGAAAAAATATATATTCAATTTTCAGGGTTGGTAACATTTTA
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT
TCTTAAGGCAACTCTCTAAATACATAAACACAACAAATTAAAATGAAAAGTGACATGAG
AGTAAATGAATCAAAAGGAAAAAACATTGAACCAGAGGTGAGGGCAGCACACCCGCAGCA
GCTGTCCAGGCCTGAGCCAATGCAACCCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG
GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTTCAATCA
GACCTGCCAAGGTGATGGGCGTCTGAGTTTCACATCTGGGCCCCCGTGACCCCACTGAG
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCACTCGTACTTGGGACAGGCCT
CTCATCTCTGGGAAGGTCCTCCTTGTTCCTACCCAACTAGAAGGGAAACAGTGGCATA
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA
GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCCACACTCC
CCACACCCCCCACACCCCCACATCCCCACCATAATTACCCCCACCTCCAAATATCTCAT

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ACCAAGTCCTCCAGCTCCTCTCCAACCAGCCCGGGAAGTTTCAGAGGATTGAAGATTTCT
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CCTGAAGGTGTGAATGGAAACCGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA
ATAGGGAAGGTCATCGGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCCTGGACAGGTAC
ACTGGAAAAGAGTTTGCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT
CTGATTGAGAACGAAGTGTCAATCCTGCGCCGAGTGAAGCACCCCAACATCATCATGTTG
GTTGAAGAGATGGAAACAGCAACTGACCTCTTTCTAGTGATGGAAGTGGTCAAAGGTGGA
GATCTCTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCACGCCA
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG
GCAGCTGGTGTGATTACATACATACTTCTCTGTGGATTCCCACCATTCCGGAGTGAGAAC
AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATTTCCAGCCCCC
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTTAGGAAATGCTTATGAAGCTGG
CCCGTGGGCTTCCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG
TGTCATCTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC
CGCGGGGACGGGGGCATGGTGTCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC
TGGCAGTTTTCCCTGTTTTCCACCACCCCACTCTTTTAATAATTGTATATAACTGTACT
TGTTCTACTTGCTTGTCTTTAAACAGGGGCCCCACAGTTCACTCTCACTGTTAGATTT
TGCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

SEQ ID NO: 26_AA383293_H

CCAGCAGCCAAGAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG
CTGGTGGTGA CTCAACGCCGCTTCCCCACCATGGAGGCCTTCTCTGCGAGGTGACATCA
GCTGTGCAGGCCCCACTGGCTGTGCGTGCCCTCTACACACCTTGTCTATGGCCACCTGTG
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

FIGURE 2S

CACAAGCTCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTTCAGGAATGGGGACCTGGTA
AGTCCCCCATTTAGTCTGAAGCTGTCCAGGCTGCCAGCCAGGACTGGGAACTGTGTTG
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG
GGGCTCCCACTGTGAGCAGGGAAGGAGCTGGTAACTGGCCATTACTATGTGGCTGTGCGA
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA
GGCAATGAAGCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCCAAGCCTCTT
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG
TCAGAAACAAGCAGAGACGGGCAATCATTCCTATCAGGAGTTATAGGAGTATATGGAGCT
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGGAACAGGTTACTTGTCTGCAA
GACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTCGTTATGCC
CAAGATGACTTTGTCTGGATCATAGTCGTCGACGGCTCCTGAGAGAGCACCAGGCGGGC
TTTGAGAAGCTCCGCAGGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA
TGTATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG
GAGCCCAAGACGAGGCCAGAAGAGAACAAGCCAGAGCGGCCAGCGGTGGAAGCCACGG
CCCATGGGCATCATTTGCCGCCAATGTGGAAGCATTATGAGACTGGCCGGGTTCATTGGG
GATGGGAACCTTTGCTGTGCTGAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCG
ATGAAGATCATTGACAAGTCCAGACTCAAGGGCAAGGAGGACATGGTGGACAGTGAGATC
TTGATCATCCAGAGCCTCTCTCACCCCAACATCGTGAAATTGCATGAAGTCTACGAAACA
GACATGGAAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTGACGCCATC
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGGACCTCAAGCCGGAACCTT
TTGGTTTCAGCGAAATGAGGACAAATCTACTACCTTGAATTTGGCTGATTTTGGACTTGCA
AAGCATGTGGTGAGACCTATATTTACTGTGTGTGGGACCCCACTTACGTAGCTCCCGAA
ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGGCTGCTGGCGTGATCCTC
TATATCCTGCTGTGTGGCTTTCCCCCATTCGCGAGCCCTGAXXGAGGGGACCAGGACGAG
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTTCTCCCCCTTACTGGGACAATATC
TCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTGGTGGTAGACCCCAAAAAGCGCTAC
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG
AAACGACAGAAGCAGGTGTCCCCAGCAGCGATGGTCACTTCCGGAGCCAGCACAAGAGG
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCAGTTCTGCTC
AAGGACAGAGAAAAGGATAGAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTCACATA
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAAAAAATTAAGT
CAATGTTAAATGTCACAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATACATTTT
TGGGGGGTAAGCATTGTCATCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC
CTTTGTAACCAAGTTTATTCTGTACTACAGGAGTGGTGCTTACCAGGGTCTAAACTCCCC
CTGTGAGATTAATAAGGTGCATTG

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ATGCCAACCGCGCCGGTCTGCGCCCGCCGCGCCGCGCCAGCGACCCCCGCCCCGCGGCA
CCAGTCGCCCCGCGCCTCCCATTCGGGGCCACCGAGGCCCATGTGACCATTCTCTGAAA
TGCTTAAGCTCGAAGATCTCTGAGAGAAAGCTGCCAGGCCCTGGTTACCTGCGGGACGA
GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGGCGTCATGCCGCTGTTTCAGCCCT
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCACTGAAGCCCAGGGTGGTGACG
GTGGTGAAGCTGGGTGGGCAGCCCCCTCCGTAAGGCCACCCTGCTCCTCAACCGGCGCTCA
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCACGCTGG
AAGAACGACCGTGTGCGGAAGCTGTTACCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT
GACTTCTTCCGGGAGGGTGATGCTTTCATAGCTATGGGCAAAGAGCCGCTGACATTGAAG
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCCCT
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCAGCAAGCTTCTGAAAGGA

FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCCAGAAG
TGGGTAAGAGGGGAAACAGGAGTCAGAACCTGGTGGCCCCGCCTTCACCCGGGGCAGCCACT
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC
GGGGAGATTGTCAGATGTGAGAAGTGTAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG
AGGGAGCCGTGCCCCGTGGGAACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
GGAGAGGAAGGGTGGAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA
ATGAGGAGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC
AGTTATCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA
GAGGAGGGGCGGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAAGCATGCC
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGGAG
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGACAGTGAG
ATTTTAATCATCCAGAGTCTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTTGATGCC
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCGAGGCTGCAGTTATGATCACAGACTTGTGT
AAGGCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC
CTCCTGGTTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGCTCCT
GAAATTCCTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC
CTATACATCCTCTTGTGTGGCTTCCCCCTTTCCGAAGTCTGAGAGGGACCAAGACGAG
CTCTTCAACATCATCCAAGTGGGCCAGTTGAGTTCTCTCTCTTACTGGGACAACATT
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC
ACGGCCGAACAGGTCTTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG
AACTCACAGAAGGAGGAGTCCCCAACAGTTTAGGTCACTTCCAGAGTCAGCACAAGAAG
GTTGCAGAGCAGATGCCATAA

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CTCCGCTGCTGTGCGCCAGGAGTCACTTCACGAGAAGCCAGGTACAAACCGTCGGCCCTTG
TCTGGAAAAGTAAAAGTGGATCCTGCCACGTTCCGAGCTCCCTGGCGCCTCGCCCGGCTG
GAGCTAGAGAACTCGTCCCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCTGGA
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCGGAGCGGTAAAAATAAGTGACTAAAGAAG
CAGACCTGGGAATCACCTAACATGTGAGGAGGAGATTTGATTGCCGAAGTATTTACAGGC
CTACTAACTACAACCTCTCAAATTTCAAATAAAAAATGGAAAACTTTAATAATTTCTATATA
CTTACATCTAAAGAGCTAGGGAGAGGAAAATTTGCTGTGGTTAGACAATGTATATCAAAA
TCTACTGGCCAAGAATATGCTGCAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT
ATTAATCTTCATGAGGTCTATGAAAATACAAGTGAAATCATTTTGTATATTGGAATATGCT
GCAGGTGGAGAAATTTTACGCCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT
GATGTTATCAGACTCATTAACAAATACTTGAAGGAGTTTATTATCTACATCAGAATAAC
ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCCTCTCGGG
GACATTAAATAGTAGATTTTGGAAATGTCTCGAAAAATAGGGCATGCGTGTGAACCTTCGG
GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACTATGATCCCATTACC
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT
TATTCGGAAGAACTTTTTCATCAGTTTCACAGCTGGCCACAGACTTTATTTCAGAGCCTT

FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA
CAGCAGTGGGACTTTGAAAACCTGTTTCACCCTGAAGAACTTCCAGTTCCTCTCAAAC
CAGGATCATTCTGTAAGGTCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC
TGTGGTGATAGAGAAGACAAAGAGAATATCCCAGAGGATAGCAGCATGGTTTCCAAAAGA
TTTCGTTTTCGATGACTCATTACCCAATCCCCATGAACTTGTTTCAGATTTGCTCTGTTAG
CACTTTTTTCTTTGACTCATTGGAAGTGAATTTGAAATTTTATATCCACTCCAGTGAGAT
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTCCATGGAATA
ATTTAGGGAAGTGTTTTAAATGTTAAATTAAGTGTGCTAGCATGTTATGATTTTCATATCC
TGAGATAGCTCTGCAGATAAGAAAATATTTAAATATATGACAAAAAGTAAAATTGTACAT
GTGAAAG

SEQ ID NO: 30_W44160_M_DRAK2_M

CCAGACGCGGCTGCACTTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG
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GAGTGCGAGGTAAAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA
GGAGATTGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCCAAAAGAACTTGCGGAGAGGAAAAT
TTGCTGTGGTTAGACAATGTATATCAAAATCAACTGGACAAGAGTATGCTGCCAAATCCC
TGAAAAAGAGGAGAAGAGGGCAGGATTGCCGGGCGGAAATTCTGCATGAGATAGCTGTGC
TGGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC
CTGAGTTAGCCGAAATGGTATCTGAAAATGATGTTATCAGACTCATTAAACAAATCCTTG
AAGGAGTTCATTATCTACATCAGAATAACATTGTTTACCTTGATTTAAAGCCACAGAATA
TACTTTTGGAGCAGTATATACCCACTCGGGGACATAAAAAATTTGTAGATTTTGGAAATGTCTC
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC
CAGAAATCCTCAACTATGATCCCATTACCACAGCAACAGATATGTGGAATATTGGCATAA
TAGCGTATATGTTGTTAACTCATACATCACCATTTGTAGGAGAAGATAATCAAGAAACAT
ATCTGAATATTTCTCAAGTGAATGTAGATTATTGAGAAAGAAATGTTTTTCATCAGTTTAC
AGCTGGCCACAGACTTCATCCAGAGCCTTCTAGTAAAGAACCCAGAGAAAAGACCAACAG
CAGAATCCTGCCTATCCCACTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTTCATC
CTGAGGAACTTCAGGCTCCTCTCAAATTCAGGATCTGACTCTCAGGTCCTCTGAAGAGA
AGACCTCCAAGTCTCCTGTAATGGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC
CTGAAGATGGCAGCTTAGTTTCTAAAAGATTTGATTTCGATGACTCCTTGCCAGCCCCC
ATGAACTTGTTCCAGATTTGTTCTGTAGCATTTTTCTCTGTGACTCATCTGGACTGACT
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT
TATAAATGCACTTCTGCTTAGAAGAACTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG
GCTAGCATATCATTTCTTGTCTGAAATTTGTTTGCAGAGGAAAATATTTAAGTATATGA
CAAAAAATGTAAATTGTGTTTAAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA
GACTTATAAAATGGGTATATTATGGTTAGTAAAGTTGAAAAAAATGAAAACAGGAAT
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAATACTCCAGAGAGAGTTTA
TAGTTGAAAGTATTTCCAGTTACCAATAATAGCTTGAAACTGTAAGATTTTCTTTGTGT
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGGTTGATCCAGGCTGTTTCTC
TGCAACCCGAGTCAAACTCGACATCATTTCCAGCTCATGTATTTTGTACGTGCATCATA
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAATAAGAGGCCTTTGTCTTCTAGA
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTGGATGTCTCCTAAGTCT
CAGGATAGAAGCCCATCATTAGAGCATAGGCACCTCAGGAATTCCTGTGTGAAATTCAG
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA
CAACACATGGGAGTGTTCAGTGTGTCCGTGGTCAATATCTATGTTTCAGTCCTGATGG

FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAGGTCTGTAATA
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA
ACAAATTAAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA
ATTGTTACTAAAATTCCAAATTCTTTAGATAACTTTAACTATTTAAATTGAGCATTGCT
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTAAAGGAAAAGTTGT
TTGCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT
GATAGATAAAATACAGCCTTTAAACAACCTC

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ATGATCCCTTTGGAGAAGCCAGGCAGCGGGCTCCTCCCCAGGCGCCACCTCAGGCTCG
GGCCGGGCGAGCCGGGGTCTGAGCGGGCCGTGCCGGCCGCGCCGCGCCCGCCAGGCCCGC
GGGCTGCTGACAGAGATACGCGCCGTGGTGCACACCGAGCCCTTCCAGGACGGCTACAGC
CTGTGCCCGGGCCGGGAGCTGGGCAGGGGGAATTTGCAGTGGTGAGAAAATGTATAAAG
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAAGAAGAAAAGGCCAAGAT
TGTCGGATGGAATAATTCATGAGATTGCTGTACTTGAAGTAGCACAAGACAATCCTTGG
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT
GCTGCTGGGGGTGAAATCTTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTTACACACTCGT
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTG
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATCTTAGTTATGATCCTATA
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTAAACATATGTCATGCTTACAGGAATA
TCACCTTTCTTAGGCAATGATAAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA
AGTTATTCTGAGGAAGAATTTGATGTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACA
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTCAAGATGGAAAAGGCACTAGAAGAAGCA
AATGCCCTCCAAGAAGGTCATTCTGTGCCTGAAATTAATTCGGATACCGACAAATCAGAA
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA
TGCAGACAGTCTGAAAAAGAGAAAATGGAGCAAAGGCCATTTCCAAACGATTTAAATTT
GAGGAACCTTTGCTACAAGAAATTCCAGGAGAATTTATCTACTGA

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CGGGGCTGCCGGGCGGGGACTGGGGGAGCCGGGCGCGGGCCGCTGCTGCCTCCGCC
CGCGCCGGGGTCCCCAGCCGCCCCCGCTGCCGTGTCCCTGCCGGCCGGCCAGCCGCGTCC
CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCCGTATCGGCTACTACGAGATCGACCG
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT
TTTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCCATATCATCAGGCTCTACCA
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTCGGAAGTTCAA
ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTCCGAACATTGTTTCATCGTGATTTAAA
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAATAGCAGATTTTGGTTTCAG
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCCAAAGTGGACATCTGGAGCCTTGG
AGTTGTCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA
TCTGCGGGCCCGCTGCTGAGTGGAAAGTTCCGCATCCCATTTTTTATGTCCACAGAATG
TGAGCATTTGATCCGCCATATGTTGGTGTAGATCCCAATAAGCGCCTCTCCATGGAGCA
GATCTGCAAGCACAAAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCCT
CTTGCCCATGGAGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA
AACCTGCGTCTCGGAGCACTTCTAGCATGCCCCGAGCCCTGGCCTTCAAGCACCAGT
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT
GATCAACCCAGAGAACCAAATTGTGGAGCCGGATGGGACACTGAATTTGGACAGTGATGA
GGGTGAAGAGCCTTCCCCTGAAGCATTTGGTGCCTATTTGTCAATGAGGAGGCACACAGT
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT
TCCTGGAGTCAACCCCCAGGCTCCATTCTGCAGGTGGCCCCCTAATGTGAACTTCATGCA
CAACCTGTTGCCATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC
TCTCCTACAGCCGCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC
ATCAGATGGAGGAGCCAACATCCAATGCATGCCAGCAGCTGCTGAAGCGCCACGGGG
ACCCTCTCCGCTTGTACCATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA
GAGCTCAGACGGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA
AAGACATACACTGGCCATGACCAACCCTACAGCTGAGATCCCACCGGACCTACAACGGCA
GCTAGGACAGCAGCCTTTCCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTCAAAGCTCACCTGGAAAAAAT
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA
CGGGGGGAGATTGATGAAAGAACCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCTCTCTCA
GCCATCTCCACCTCTTCAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT
CCAGAGGTTAAGGATTAGCCTTCAAGCCCCACCCCCAACACCCCAACAACCATCTCTT
CAGGCAGCCCAGTAATAGTCCTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC
TGATCTTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC
TGAGAACTGTTCTCTCTCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC
TCAGTCACAGCAGGTACCATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT
GCAGATGCAGCACCGTACCAACCTGATGGCCACCCTCAGCTATGGGCACCGTCCCTTGTC
CAAGCAGCTGAGTGCTGACAGTGACAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTTCGACCAGTCCCGGGGTTCT
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCCAAGCCCTGAAAGT
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGACATCAGCAGCCGCCACACTA
TACCAGTCGGCACTACAGCAGGCCCTGCTGTCTCCCACGCCGCCAGACTATAAAGACA
CCAGCAGGTACCCACATCCTTCAAGGACTGCTTTCTCCCCGGCATTCGCTCACCGGCCA
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGACAGCTCATTAAGGAGCAGCAGCAACA
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAAATACCAGGAACTGTTACGGCACAT
GAACCAAGGGGATGCGGGGAGTCTGGCTCCCAGCCTTGGGGGACAGAGCATGACAGAGCG
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT
GCTACAAATCAGGGCACAAGAATGTGTCTCAGAGGCTTCTCACCACCCCCGCCCCACGG
GTATGCTCACCAGCCGGCACTGATGCATTAGAGAGCATGGAGGAGGACTGCTCGTGTGA
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAGGTTGCCA
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCCTGAATCTTTGCTAGGAAC
TGTGAGTCATGCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAAGTCTGCTGCTT
CAGTAAAAATAAGGTGCCAGCAGAGAGCCTGTGATAGGGAAGTGCATGGATAGAAGTTC
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCCCTC
CGTCCATAGACACCACAGGCCCCGGGCCCTCCAGAGACACCACACGATCCAGAACAGCGA
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT
TAGCTCTGCCCCGATGTGCGATGCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTCATGAGCACCCAGA
CCTGAGTGATGCGAGCCAGCATTTAAACTCCTCTTGCTATCCATCTACGTGTATTACAGA
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTCAGCATGGAGCAGGCAGGCGTGTA

FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC
TGCTTTCCCTCACATTGGTTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC
CATGTTTGCTTGTATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC
C

SEQ ID NO: 33_2R22-5-11_H

CTGGGCCGCTGCCGGTCAGGTCGGCCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG
AACCAGCCAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTTCATCTAAATAAAGGCC
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT
TATTTGCAAGTTTCTTCTTCTGCGGTCCAGATTATTAGGTCTCCAGCGCCCTGCAGCT
TGACAGAAAGAGAAGCATGAAATGAAGGTCAGAGATGAGATCCCGCAGCAGGGACGTGGG
GGCCTCCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG
CAAACAGAAGCCTTTGTCTCTGGGGCACAGCCACCTACCACAAAGCATCAGACTCCACGTC
TGGCCAGAAAGTTCTTGGAGTCCCATCAGGCCAGTGCGGTATGTAACATGTGCCTAATTGT
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCCTCTCACTAAA
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACCTCTTTGAACCCTGGGCACCTGCTGT
CCTCAGTTGGCATCTCCACCCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG
CTGAGATGGAGACGTGAGCCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC
CTGGTGAAACCCCACTATGCCCCGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTGAG
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA
CTGACACAGGACATGTCCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG
ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAACCTTCTCCCAAGTGAAGCTT
GGGATTCACTCCCTAACCAAGAAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA
GACCAGAAAACCCAGAGGCTACTATCCCGAGAAATCTCCAGCATGGAAAAGCTGCACCAT
CCCAACATCATCCGCCTTTACGAAGTGGTGAGACCCCTATCCAAGCTGCACCTTGGTGATG
GAGTATGCAGGGGGTGGGGAGCTCTTCGGAATAATTAGCACTGAGGGGAAGCTCTCTGAA
CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC
CAAATTATTCATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG
AAGGTGGGCGATTTTGGATTACAGCACAGTAAGCAAAAAGGTGAAATGCTGAACACTTTC
TGTGGGTCTCCTCCCTACGCTGCGCCTGAACTCTTCCGGGACGAGCACTACATCGGCATT
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGACTGGCACCATGCCA
TTTCGGGCAGAAACCGTGGCCAACTAAAAAAGAGCATCCTCGAGGGCACATACAGTGTA
CCGCCGCACGTGTCAGAGCCCTGCCACCGACTCATCCGAGGAGTCCTTCAGCAGATCCCC
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC
CCTACACCTTTGGAACCTTTCCAACCTGGATCCCAACATTTGTTCGGAACCCAGCACTCTC
AAGGAAGAAGAAAATGAGGTCAAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT
ATTGAAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCCAGTCATGATGCTACCAGAC
CCTAAAGAAAGAGACCTCAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC
AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACCTAACCAAGATGATTGTT
GCTGCTTCTAAATTTTTTTCAAGGACAACCTGAGTGAGAGACATTTTTGTAAATTTTTAAAT
AAACTTAAATTTGAGATATGCAAAAAA

SEQ ID NO: 34_R31237_1_H, AAC33487

ATGTCCACTAGGACCCCAATTGCCAACGGTGAATGAACGAGACACTGAAAACCCACACGTCA
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAACTACAGACTGTTGAAA
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAAAATTGGCAAGACATATCCTTACAGGCAGA
GAGGTTGCAATAAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTTCGAA
GTCATTGAAACTGAAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA
TTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAAATAGCAGATTTTCGGTTTTAGC
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAGTCTTCCATACGCAGCA
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAGTGGATGTGTGGAGTCTGGGG
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCTTCTACATGTCTACAGACTGT
GAAAACCTTCTCAAACGTTTCTGTTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTTGTT
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT
TCACAAGAAGAAATTCAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA
TATTTGTTATTGGGGAGAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTCTTAGCAGC
AATCTTTCACCTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT
CCTCACCACAAAGTGCAGAGAAGTGTCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC
CATGCTGGACCAGCTATTCCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTTCCCGGAAATCAAGTGGCAGTGCTGTT
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG
GCGGATATTCCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT
GGAATGACACGACGAAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA
GTGATTGAGAATGGCAAAGAAAACAGCACTATTCCTGATCAGAGAACTCCAGTTGCTTCA
ACACACAGTATCAGTAGTGCAGCCACCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC
AGTCGTAGCACTTTCCACGGCCAGCCCCGGGAACGGCGAACCGCAACATATAATGGCCCT
CCTGCCTCTCCAGCCTGTCCCATGAAGCCACACCATTGTCCCAGACTCGAAGCCGAGGC
TCCACTAATCTCTTTAGTAAATTAACCTCAAACCTCACAAGGAGTCGCAATGTATCTGCT
GAGCAAAAAGATGAAAACAAAGAAGCAAAGCCTCGATCCCTACGCTTACCTGGAGCATG
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAAGTGTTGGAC
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT
GGGCACGCGGAGAACCTCGTGCAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT
CTGAACGGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

SEQ ID NO: 35_W90839_M

AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCCTTGCCGGAACCTCTATCGCTTCC
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTGCTATTAAG
ATCATTGATAAGACCCAGCTGAACCCCACTAGCTTGCAAGAGCTGTTTACAGAGAAGTCCGA
ATTATGAAGGGACTCAACCACCCCAACATCGTGAAGCTTTTTGAGGTGATAGAGACGGAG
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTGACTACCTCGTG
TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTCAGCC
GTGCACTACTGTATCAGAAGAACATTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG
CTGGATGCCGAGGCCAACATCAAATCGCCGACTTCGGCTTCAGCAATGAGTTCACGCTG
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATAAGCCGCCCCAGAGCTGTTCCAG
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTATCCTGTACACG
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC
CTCAGAGGAAAGTACCGGGTCCCCTTCTACATGTCTACAGACTGCGAGAGCATTTCTGCGG

FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG
CGGATGCCGGGTCGGAAAGCGAGCTGCAGTGCAGTGGGCAGTGGAAAGTCGAGGCTTGCCC
CCCTCCAGCCCCATGGTCAGCAGTGCCCAACAACCTCCCCCCCAGCATGATGACCCGAAGAAAC
CGGAAGGACAGCACTAGCACCCCTAACAACCTCCCCCCCAGCATGATGACCCGAAGAAAC
ACCTATGTGTGCACAGAGCGACAGGATCTGAACGCCCCGTCTTGTGTCCAAATGGCAA
GAAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCCTGGCT
CCCCCGTCAGGCGAGCGGAGCCGCCCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGTGTGCAGAAATGGA
CCCCCAGCCTACCCACGCTTGCCACGAGGCGGCACCCCTGCCCTCCGGGCGGCCCTCGC
CCCACCACCAACCTCTTACCAAGCTGACCTCCAAACTGACCCGAAGGGTCACAGACGAA
CCTGAGAGAATCGGGGACCTGAGGTCAAGTTGCCATCTACCTGGGATAAAACGGAA
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

SEQ ID NO: 36_406786.5_H

GTAGCCGGCTTGGCGTGACCGTCGCCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT
GGCCTCCCTTCTTCCCATGGAGGTGCGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG
CCTTTCCAGAGCCTCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC
TGAGCCAGCAGGTGTTTTCTCAGCCACAGACACCTGAGCAGAAGGAATGGGCTTTC
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC
ATCACTGGCTGCCAGAATATTTGTACAAGTAAACTGCACTGCCCTGCTGCCCTGAGCA
CACGGACCCGTCCGAACCGCGGGCAGTGTGTCTGCTGCTCCCTGCTGCGGGGACTGTC
CTCAGGGTGGTCTCACCTCTGCTTCCGGCCCCCTGTGTGCAACCTAACAAGGCCATCTT
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTCAGA
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT
GGTGTGTTGGCACGGTGGTGGACATCATACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCTATGCTGCGTGGTGGTCTGAGACCCGT
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTGATGTGACAG
TCTCTTTGCTCATCTTACCGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA
GATTCAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGCCCTGTGAGCGGCTA
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCTCCTGCCGATGG
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAGACGGA
GCTCCTGGGCAAGAATATCACTTTCTGATTCTGTTTCTACAGCTACATGGACCTTGC
GTACAACAGCTCATTACAGCTCCCAGACCTGGCCAGCTGCCTGGACGTGCGCAATGAGAG
TGGGTGTGGGGAGAGAACCTTGGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA
GGATCCAAGGATTAATGTGCTGCTTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG
GAAGCTGATGGAAAGCCAAGACATCTTACCGGGACTCAGACTGAGCTGATTGCTGGAGG
CCAGCTCCTTTCTGCCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCCAGAAGG
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC
TGAACCAAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC
TGAGGATGGGGGAGTGATGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG
GATGGGAGTCAGTGGTCCCAGCGGTTACAGCCTTTGGGCTGGGGCTGCCGTGGCCAAGCC
CCAGGCCAAGGGTCAGCTGGCGGGGGCAGCCTCCTGATGCACTGCCCTTGCTATGGGAG
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCCTTGGGATGGCAGG
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAAAACGACCGAGA

FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGACAGGAGCCCT
GGATGTCCCCCAGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG
CTATGCCTTGGCCACGGACCTCCCTGGGGGCCTGGAAGCAGTGGAGGCCAGGAGGTTGA
TGTGAATTCGTTTTCTGGAACCTCAAGGAACCTCTTTTCAGTGACCAGACAGACCAAAC
GTCATCAAATTGTTCTGTGCTACGTCTGAACCTCAGAGAGACACCCTCTTCTTGGCAGT
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCGTGTGTCCTGGATGACAG
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGCCCAAGGCCGACGGTTCCGGGA
GAGCTGTGTGGGACATGATCCAACAGAACCGCTTGAGGTTTGTGTTGGTGTCTCTGAGCA
TTATGCAGCAAGCGACAGAGAAAGCCAGGACACGTTCTTCCACGTTGGATGCTGGCCC
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCACGTTACCTCCACGCC
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGGTGCCTACTC
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAAGACCTCCTCCACAG
CCAACGCGACTCAGCCGCCAGGACCCGCTGTTCTTGCCAGCCTGCCCCGCTCCACCCA
CTCTACCGCTGCTGAGCTCACCGGACCCAGCCTGGTGGAAGTGCTCAGAGCCAGACCCTG
GTTTGAGGAGCCCCCAAGGCTGTGGAACCTGGAGGGGTTGGCGGCCTGTGAGGGCGAGTA
CTCCCAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC
TGCTGTGGACAAGGGAAAAACAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT
CTTGAGGATTGTTGGATTGAGGATCCCAAACCTTGGGAAAGTTACTTTAGAGATCGCAAT
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA
CCGCCACCCAGGCTGGATGAGCCCCCTGGCGAGCTACATCTCCGACAAGTGAGAGCAGG
CCAGAGCCGTCTAGTGTGAGCAGTGGGATACCTGCGCTTGAAGGACATCATCCACCGTGA
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG
CTCGGCCGCTACTTGGAAGGGGAAAATTATTTTATACTTTTTGTGGGACCATCGAGTA
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCTTCTGTGAGCTGGAGGA
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCAAAGAACTCATGAGCCTTGT
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA
CCCGTGGGTAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT
GAGTGATGTGGCCAGGCTCAGGAGCTTTGTGGGGCCCCGTTCCAGGCGAGGCTCCTAA
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCGTCTGCTGACCAGCTAAACACCAATTTCT
TTCCTGCTTTTCTCCACTTGGTTTGGAAAATCACACAGTTTTTCAGGCTCCATCTGTTTG

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CCACGCGTCCGCATCCCTGCTTGATGAGCCCTGGCGAGTTTCATCTTTCGACAACCTAG
TGTCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA
ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT
TAGAGAGGGGCAAACTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTACCC
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG
TTATTCATCCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC
AGCCTTGCCCTGAGCAGCGGACCACTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA
GTGGCCTGCTGTGAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCAGGGAGACTCGTGGTGACCAGCACTGCT
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG
GGCAGTTGTATGGATTTAGGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

FIGURE 2BB

TGACTTCTGCTTCTAGATTCCCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT
AGGTTTTATGATATAGACTTGTAATTCATGTTTTTTTTATAACCTTGAAAATCATTCTAATG
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG
TGTTTAAGTTCTCTATTTTTTGTGTTTGTGTTTTTGCTTGTAAGTTTTTGAGACAGGATCTC
ACCATGTAACTTTGGCTGGCCTGGAACCTCACTATGTAGACCAGGTAGACCTTAAACTGA
CAGATCTGCCTGCGCTTGCCTCCCAAGCATTAGGACTGATGGTGTGTGTCAACCATGCCCA
GTTCTTCTGTTTTTGTGTGTAGGTTTCTTTCCCACTGACTTGGTACATGTGACATGTGA
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAATGGCCAGAATATTTATTTATTTT
CTTAAAAATTTTCCAAATTAAAGCTACTTAGTTAACAGTTAACTGGCCAGGACTATATG
AGATAAACTTGGTTTTCTATTTCTTTTTGT

SEQ ID NO: 38 AA785735_H

GGCACGAGGCGCGCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA
GCAAGCGGAGCGCAGTTGCCCCAAGCCAAGCCGCGCTGCCAACCTCCCGCCCCGCCGCG
CTCCTGTCCGCCGTGTCTAGCAGCGGGGCCAGCATGGTCATGGCGGATGGCCCCGAGGCA
CTTGACGCGCGGGCCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACTTTATCAGGTAATGGAGACCAA
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAATTTTTGACTATCTTGC
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTTCTGGCAAATCCTGTCTGC
TGTTGATTATTGTCTATGGTTCGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT
GCTGGATAACAACATGAATATCAAAATAGCAGATTTGCGTTTTTGGAAATTTCTTTAAAAG
TGGTGAAGTCTGGCAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT
TCTGGAAGGAAGATTCCGGATTCCGTATTTTCATGTCAGAAGATTGCGAGCACCTTATCCG
AAGGATGTTGGTCTTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA
ATGGATGCTCATAGAAGTTCCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA
TGAGCCATCCATCGGGGAGTTTAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAT
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAGAGCTATAACCACTTTGCTGCCAT
TTATTTCTTGTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGGAGCAGAG
ACTTGATGGCCGCCAGCGTCGGCCTAGCACCATTGCTGAGCAAACAGTTGCCAAGGCACA
GACTGTGGGGCTCCCACTGACCATGCATTACCGAACATGAGGCTGCTGCGATCTGCCCT
CCTCCCCCAGGCATCCAACGTGGAGGCCTTTTTCATTTCCAGCATCTGGCTGTGAGCGGA
AGCTGCATTTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA
CCCTGTGCCTCCTGTCTGGTGCAGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCGGAGGAAGACCCCCGCTCATGC
CTTTGAGGCATTTTCAGTCCACACGCAGCGGGCAGAGACGGCACACTCTGTGAGAAGTGAC
CAATCAACTGGTTCGTGATGCCTGGGGCAGGGAAAAATTTTCTCCATGAATGACAGCCCCCTC
CCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTTCAGAGGGACCTGAACTTTCT
GGAAGACAACCCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCAGAA
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGAGAGCATCAGATAC
CTCCCTCACCCAGGGAATTGTAGCATTTAGACAACATCTTCAGAACTTGGCTAGAACCAA
AGGAATTCTAGAGTTGAACAAAGTGCAGTTGTTGTATGAACAAATAGGACCGGAGGCAGA
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCAGCCT
TCTGTCAAAGGCCCAGAACACCTGTCAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA
ACTGCAGGCCTATTTTAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA
GCAGCTGCCCCCTTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTTCAG
CCTGACCCAGCCCCCTGAGCCCCGTCTGGAGCCTTCCCTCCGAGCAGATGCAATACAGCCC
TTTCTCAGCCAGTACCAAGAGATGCAGCTTCCAGCCCCTGCCCTCCACTTCCGGTCCCCG
GGCTGCTCCTCCTCTGCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG
TGAGCTGCCAAGCGCTGCTTCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCAGAAGCCCAGGACTGCA
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCCTGGTGAATTAGTCTCA
GCACAGGAATTGAGGTGGGTGAGGTGAAGGAAGAGTGTATGTTCTTATTTTATTCCAGC
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCCCTCCTGGTTCTGCCCCACCA
CAAAGTTTTCTGTGGCAAGTGTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG
AACCCGGGAGGCGGAGCTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCG
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGGCAG
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA
TTTTTGTCTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC
ACTGGGGCACAGATAGAGAACCAGGCGGCAGCAGTGTCTGCAGACCCACCCAGGGAGAGC
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT
TTGTACATTAGTTTTTACCAAGCACTTTCTCTTCTAACCTCACAACAATTCTATGAAATT
AGCTGGGGAGATACTGTCCTTATTTTTTACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTTGAC
TGGCTTCTGGTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTCCCTTCT
CTTTCCTCAGTAGCATCTGACTCTTTTTCATAAGCAAACAGCTGTATAAACAAAGCCCCCA
TTTTTGGTCAAGCACAGGTGAATGTGATATTGTTCCCACAACCTTATTCTCCACTCAACA
GCCGCTGGCTTTGGGGAAGAGGCCCTTTCAGGTGACAGTGCAGCTGTCCAGGTGGCCG
TGCCTGAACCAGGCTGAGGGAGACAAAAACCCGAGACCCGCTGCCTTTCAGCGTCC
AGTTAACTGCAGAAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC
AGCAGTTTTCTACAGAACACCCCTTCTCAATTGCCAAGGGGCCGATCGCACGGCATC
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCATGAACTCAGCCTTTGT
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGCCCCATCACTAGAAGTGCTTATTA
CTTTTAGGATTAAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTTCAGAGGCA
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT
ATGACCCAGATGGAATAATGTCACATTCCCAAGTGCAGATAATGGGCTGCTGCTGGCTC
TGTGGTGTCTGTCTGCAGAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC
CACCATGGGTGGTAAGAGAAACCTGCCTTCACCAAAATCTCTGAAGGGGAAAGAAGTGGA
GAGAAAGTTTGTCTCACTTCGGGGACTGCAGTTTGAAGAAATAAAGGGATACAGAGATA
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT
TTTCTGTGTGCTTTTTTTTAACTACTAAGAAAAAATTTGGTGAGTTTCAGTAGCTTTGGTA
TTATGAGTGCAAAATCATAATAGCTCCAATGTGAAAAAATAATCAAAAGTATAACTTGTC
ACTTAATGTTAGAAAATTGCCTAAAATGCAGTGTAATAAATAATCTCTGTACCAAATAGT
AATTTAAATGGGGTAATTTTCTGCAAGGAAATGTACTGTTTTTATGTTTCCAACCTCT
TGA

FIGURE 2DD

SEQ ID NO: 39_AA207220_H

GCTGTGGCTCCCCGTCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC
CTATTGATTCCTGCGCCCTTGCTCCACCTCTGCTCGCCATGGAGTCGCTGGTTTTC
GCGCGGCGCTCCGGCCCCACTCCCTCGGCGCAGAGCTAGCCCGGCCGCTGGCGGAAGGG
CTGATCAAGTCGCCCAAGCCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG
CACAACCTGCGGCACCGCTACGAGTTCTGGAGACCCTGGGCAAAGGCACCTACGGGAAG
GTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCA
CTCAACCACCCTCACATCATTTGCCATCCATGAAGTGTGAGAACAGCAGCAAGATCGTG
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCGGCAGATCGTCTCTGCCGTGCACTATTGC
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCTCTACATCCTGGTGCATGGC
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC
TACCGGGAGCCACCTAAACCCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG
GTGAACCCACCCGCGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT
GACTCTGCCCCGCGCTCCATGGCTGACTGGCTCCGGCGTTCTCCCGCCCCCTCCTGGAG
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC
CCTGGCCTGGAGCGCCAGCATTCTGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCAG
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGAC
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCAGGGCAGGCTGCCCCCTGCTCCCCAAG
AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCC
AGTGAATCTGGGGAGCTCTTGAGCGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT
GGCAAGTTCTCCAGACAGCCTTGAGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT
GAACTCGCCCCACCTCGCCCCCTGGCCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG
GACAGCATCCTGTCTCTGAGTCTTTGACCAGCTGGACTTGCCTGAACGGCTCCAGAG
CCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCTCA
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGACAGCTGCTTT
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCGGTCAGGCTCTCAGATGCAGCTGG
TTGCACCCCGAGGGGAGATGCCTTCTCCCCACCTCCAGGACCTGCATCCAGCTCAGA
AGGCTGAGAGGGTTTGAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG
AAATGCGCCAAGGGTTCAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA
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GGCCACAGAGA

SEQ ID NO: 40_AA426580_H, MAK_V_H

ATGCCGGCGGGCGGGGACGGGCTCTGGGGGAGCCGGCGGCGCCTGGGGGCGGGCGG
GGCGCGGAGGACGCGGCCAGGCCCGCGGCGCTGCGAGGGAAGTTTCTGCTGCTGG
GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCCAGCACCACAAGCGCGTGGGCAAC
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG
GACACCTATGTACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC
CCCAATATCACTCAGCTCCTTGATATTTAGAAACGGAAAACAGCTACTACCTGGTCATG
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

FIGURE 2EE

TCCGAAGCCCGCAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC
AAGCTGATTGACTTTGGTTTGAAGCACTGCGCAGGGATCCTGGGTACTCGGATCCGTTT
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG
CTGCCCTTTCACGGTGGAGCCTTTCAGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA
GAAATGAACCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTGCGCTCTCTC
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTTCAGCAGGCACTGGCGAATCGCTGGCTT
AATGAGAATTACACGGGCAAAGTGCCCTGTAATGTACCTATCCCAACAGGATTTCTCTG
GAAGATCTGAGCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC
GACGTGATCAACACTGTGCTCTCCAACCGCGCCTGCCACATCCTGGCCATCTACTTCCTC
TTAAACAAGAACTGGAGCGCTATTTGTGAGGAAATCTGACATCCAGGACAGCCTCTGC
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCCTATGAGGCC
TCTCTGGACACCTGGACACGAGATCTTGAATTCATGCCGTGCAGGATAAAAAGCCCCAA
GAACAAGAAAAAGAGGGGATTTTCTTCATCGACCATTCTCCAAGAAGTTGGACAAGAAC
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTGAGAACACCAAAGCC
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCTTTGGCTGC
CGCAATATTTTCCGAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTTCATGGAGTTC
ATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA
GGGCCCCGAAGCACTGGCATCCCCACAAGGAAGACCCCTGATGCTGGACATGGTGC GC
TCCTTCGAGTCTGTGGATCGCGACGACCACGTAGAAGTGCTGTCTCCCTCTCATCTACTAC
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCCAGCGAGAGGACGCTGTCC
CCGGGTCTGCCATCCGGAAGCATGTGCCTCTCCATACTCCTTTGCATCCAATCTGGTC
TCTTTTGCTCACGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT
CCGGTTCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA
GGCCGTTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCCACTGCAGCCCCTAGCCCCTGTG
AACCTTGCCTTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

SEQ ID NO: 41_Z36720_H

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GACACCCAGGCTGGGTGGCCCGAGGTCTGGAGCTGGTGAGGGCCATGCAGCAGGATGCG
GCCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAGGATGGTGGCTGCGGTGGACAGGGCC
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTCATGCAGGGG
CGTGTGCCCTGGAGGAGAGGCAGCCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG
AAGGATAAGGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG
ATCATGGTGACAGCGGCAAAATAAGAGCGAGTGGAAGAAGAGGGAGGAAAACCAAAGCAT
GTGCTGAGCACCAAGTGGGGTGCACTCTGATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA
GCTGACCCCGCCAGGCAGTGGTCTACCGGGCCAGGGAGATGGTGTCTCTGGCCAGCC
CAGGCATTTCCCTGGCCACCTGCCCCCTGCCACAAAGGTGGAAGCCAAGGCTCCTGAGACA
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG
GTCTCCCCGAGCCTGGAGGTTGCACCAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT
GACCCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA
GGGCCTCCAGGGCTGCCAGCCAGGCCAGGGCAACCCACAGTGGTGGAGAAAACCTCCA
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGT
CTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGCAGCCTTGGACCCACCCTCACCACAGAGGCTCCA
GCAGCTGCCCAGCCAGGCAAGCAGGGCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCT
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCGCTGCAGGAG
AGCAGCAGCCCCGGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG
CAGCAGGGCAAAGCCCAGGGGCGGGAACCCCTGAGCCTGAGCAGGACTGTGCAGCCAGG
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCAGGCGCCGAGGCTGGCAGCGTG
GTTCTGGATGACAGTCCGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTCCG
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCTTCGAGAGCAAGCACAGCTGC
ACCCTTGTCATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG
TACCACCTGACTGAGCTGGATGTGGTCTGTTCACCAGGCAGATCTGTGAGGGTGTGCAT
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT
CGAGAGAAGCTGAAGGTGAACCTTCGGCACTCCTGAGTTCCTGGCCCCAGAAGTCGTCAAT
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTCATTGTA
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC
TTTGTTCCTCGGTTGCTGGTCAAAGAGAAGAGCTGCAGAATGAGTGCCACACAGTGCCTG
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAA
TCCCCAATACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACCTTCTCCCTAA

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CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCGGCTGACCGTGCGGCCCTCG
TTGGCACCCCTGTTTACACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC
CGTTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC
TGCCCCATGGAGGAGAGTGAGAACTTGCGGCTGCGGCAGGACGGGGGTCTGCACTCACTG
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTGAGTGTGTTAACACC
CATGGCCAGGCCCACTGCTCAGCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCCTCA
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG
CTGGAGCGGTGTCCATTCCCGACTTCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCACCATCAGCTGG
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT
GTCCATCGCTTGGTGTTCCTGCCGTGGGGCCTCAGCACGCCGGTGTCTACAAGAGCGTC
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCACCTGTATGTACAGATGTGGTC
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGACTCCCTGACGTACACA
GTGCAGCACCAGGTGCTGGGCTCGGACAGTGGACGGCACTGGTCACAGGCCTGCGGGAG
CCAGGGTGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCTCAGC
ACCACTGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGGAG
CACGGCCCCAACCTGGAGGAGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG
GTGGAGGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGGCCAGGTGCTC
TGGAGGAGCTGCCGAGGGGCCCTCCTAGAGGCACGGGCGGTGTGTACGAGCTGAGCCAG
CCAGATGATGACCAGTACTGTCTTCGGATCTGCCGGGTGAGCCGCCGGGACATGGGGGCC

FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTCACGGCACACAGACCTGCTCGGTACATTGGAGCTG
GCAGAGGCCCTCGGTTTGAGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAACT
GCTCGCTTTGCGGTGGTGGTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC
CTGGTGGTGTCTCAGCACGGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCAGAAC
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTTCAGCTCAGACAGCTATG
GAGGTGAGGGGGTTCGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCTACTTGCGGCGCATAGTGAGGCGT
AGCTCCGGCCTGGAGTTTGCGGCCAAGTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA
GCGCGTCGGGAGGCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT
GAGGCCTTCGAGAGGCGCCGGGACTGGTCAATTGTACCGAGCTCTGCACAGAGGAGCTG
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG
CAGGTGCTAGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG
CCTGAGAACCTGCTGGTGTGGGATGGTGTGCGGGCGAGCAGAGGTGCGGATCTGTGAC
TTTGGGAATGCCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT
GAGTTTGTAGACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG
CCTGTGGGTGTTGTTGCCTTCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAAT
GACCGGACAACATTGATGAACATCCGAACTACAACGTGGCCTTCGAGGAGACCACATTC
CTGAGCCTGAGCAGGGAGGCCCGGGGCTTCCTCATCAAAGTGTGGTGCAGGACCGGCTG
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTTCAAACTCAGGCAAAGGGCGCA
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCCCGCGGAGGTGGCAGCGCTCCCAG
ATCAGCTACAAATGCCACCTGGTGTGCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCCA
GAGCGGGTGTGGGTGACCATGCCCAGAAGGCCACCCCCAGTGGGGGGCTCTCATCTCC
TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCCCACTGCAGCCC
GAGTTCTCTGGCTCCCGGGTGTCCCTCACAGACATTCCTCACTGAGGATGAGGCCCTGGGG
ACCCAGAGACTGGGGCTGCCACCCCCATGGAAGTGGCAGGAGCAGGGAAGGGCTCCCTCT
CAGGACCAGGAGGCTCCCAGCCCAGAGGCCCTCCCCCTCCCCAGGCCAGGAGCCCCGAGCT
GGGGCTAGCCCCAGGCGGGGAGAGCTCCGCAGGGGCAGCTCGGCTGAGAGCGCCCTGCCC
CGGGCCGGGCCGCGGGAGCTGGGCGGGGCTGCACAAGGCGGCGTCTGTGGAGCTGCCG
CAGCGCCGAGCCCCGGCCCGGGAGCCACCCGCTGGCCCGGGAGGCCTGGGTGAGGGC
GAGTATGCCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGAGGCCCCGAGGAT
GGCAAGGTGAGCGGCCTCAGGGGTCCCTGCTGGAGAGCCTGGGGGGCCGTGCTCGGGAC
CCCCGGATGGCACGAGCTGCCTCCAGCGAGGCAGCGCCCCACCACCAGCCCCCACTCGAG
AACCAGGGCCTGCAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG
CACCGCCGAGCGGGGGCGCCCCCTCGAGATCCCCGTGGCCAGGCTTGGGGCCCGTAGGCTA
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCAGCCATCCAGCCCTGCACGGCCC
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT
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TCGCAGGGCCCTGCCGCGCCCTTCCAGAGCCCAAGCCCCACGCTGCTGTCTTTGCCAGG
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GAGTCGCCCCGTGCTGCTGGGGCTGCGGCTGCTGAGCCGTTTCGCGCTCGGAGGAGCGGGC
CCCTTCCGTGGGGCCGAGGAGGAGGATGGCATATACCGGCCAGCCCCGGGGGACCCCG
CTGGAGCTGGTGCACGGCCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTGGA
GAGCCTGGCTCGTCCGCGCCCTCTCGCTGTCACTGTCCAGCGGCTGCGGCGGACCCCT
CCCCGCGAGCGCCACCCGGCCTGGGAGGCCCGCGGGGACGGAGAGAGCTCGGAGGGC
GGGAGCTCGGCGCGGGGCTCCCCGGTGTGCGCATGCGCAGGCGGCTGAGCTTCACCCTG

FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCTG
GGCCGAGCACGCCGCTGTTCCGACGGCTTCGCAGGGCCACGTCCGAGGGCGAGAGTCTG
CGGCGCCTTGGCCTTCCGCACAACCAAGTTGGCCGCCAGGCCGGCGCCACCACGCCTTCC
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTCTGGGCTCCTCAGCCCCAGGGGAAAGC
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTATCGCCACCA
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTCAACAGTACGTGCGCAGTGAGTCAGAC
TTCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGGAGGCAGCC
ACCCTGCTCTGCCTGCCAGCGGCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG
AAGTCCCTTGAGGTGAGAGCCCTCAGTGATCATCGTGTCTCTGCAAAGATGGGCGGCAGCTG
CTCAGCATCCCCCGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCGAGTCCCAGGAAAGCTA
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGCTGTGGAAAGCCGGGA
GACAGCCGGGCACCTTGACGTATACGCTGGAGCGGCGAGTGGATGGGGAGTCTGTGTGG
CACCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCGTGCTGGGCAGGGGGCCCTTCAGCAAC
TCTTCTGAGAAGGTCTTTGTGTCAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGCTGCC
CACCAAGAGGGCCCTGTACCTCAAGGCCAGCCAGGGCCCGGCCTCCTGACTCTCCTACC
TCACTGGCCCCACCCCTAGCTCCTGCTGCCCCACACCCCGTCAGTCACTGTCAGCCCC
TCATCTCCCCCACAACCTCCTAGCCAGGCCTTGTCTCTGCTCAAGGCTGTGGGTCCACCA
CCCCAAACCCCTCCACGAAGACACAGGGGCCTGCAGGCTGCCCCGCCAGCGGAGCCCACC
CTACCCAGTACCCACGTACCCCAAGTGAGCCCAAGCCTTTTCGTCTTGACACTGGGACC
CCGATCCCAGCCTCCACTCCTCAAGGGGTAAACCAGTGCTCTCCTCTACTCCTGTGTAT
GTGGTGACTTTCCTTTGTGTCTGCACCACCAGCCCCCTGAGCCCCCAGCCCCCTGAGCCCCCT
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCGGCCAAGGAGGTGGTCAGCTCC
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCTGAGGGTACCACTCTTCGACAGGGTCCC
CCTCAGAAACCCTACACCTTCTGAGGAGAAAGCCAGGGGGCCGCTTTGGTGTTGTGCGA
GCGTGCCGGGAGAATGCCACGGGGCGAACGTTCTGTGGCCAAGATCGTGCCCTATGCTGCC
GAGGGCAAGCCGCGGGTCTCTGCAGGAGTACGAGGTGCTGCGGACCCTGCACCACGAGCGG
ATCATGTCCCTGCACGAGGCCTACATCACCCCTCGGTACCTCGTGCTCATTGCTGAGAGC
TGTGGCAACCGGGAACCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC
GTGGCCACTTACATGGTGCAGCTGCTACAAGGCCTGGACTACCTCCACGGCCACCACGTG
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GTGGACTTTGGCAGTGCCAGCCCTACAACCCCGAGGCCCTTAGGCCCTTGGCCACCGC
ACGGGCACGCTGGAGTTTCATGGCTCCGGAGATGGTGAAGGGAGAACCATCGGCTCTGCC
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTT
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCCGCTTTGATGCCTTC
CAGCTGTACCCCAATACATCCCAGAGCGCCACCTCTTCTTGCGAAAGGTTCTCTCTGTA
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CGGTTACCACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA
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TCAGGCTCAGCAGGTTGGGAACAGGCAGAGGGACAAGAGGGGAATGGAGAAGTGAGAGG
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTTGGGGGTGAGT
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC
CCAGGTGTCAGGGCAGTAGGCTGGGAGTCAGTGTGGCAAAGCGGGGGCAGGACACAGATA
CAGTGGCAGGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGGCGGCAGAGGGAGAAG
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGTGTGAGCATCCCTCAGAGGAGAAATGTG

FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCTCCTGTCCAGTGGATACAGC
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCCTCCATGGCCTTTGGCCTTCT
TCCCATTCATATTTATTTATTTATTTACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT
ACTGCCCATGTTGTCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA
AGGAAATAAAAATGGCAAGCAGCAAAAAA

SEQ ID NO: 43_AA542015_M SGK088_M

GCCACGGACATCTGGGGAGCGGGTGTGCTCACCTACATCATGCTTAGTGGGTACTCCCCA
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGGTCGCTTTGATGCC
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGTCTCTCA
GTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCCACCCATGGCTGCAAGAT
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTCACCACCAACCGGCTCAAGGAA
TTCTTGGGCGAGCAGCGGCGACGTGCGGCTGAGGCTGCTACCCGTCAAGGTGCTGCTC
CGCTCCTACCCTGGCAGCCCCCTAGGTGGCACAGACCGCAGCCCCGCCACGGGCTTCAACT
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTCACCCCGGCCATA
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAAGA
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT
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AAGAAGGACCCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC
CAGGAGCCAGAGCAGAGACATAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAAG
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC
ACTGGCCCAGGGATGTCCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCATTTGTAT
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SEQ ID NO: 44_R19772_H

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AAGAGCTTTGACCTGGGATCTCCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCACACACACCC
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GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGATGAGCTGGTA
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ATAGAAGAAAAGGGTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTTTGGAAAT
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CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCCTAC
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGAAGTTCCTCATCAAG
CCCATTTCAGAGAATAACAAAATACCAGTTGCTCCTCAAGGACTTCCTGAGATACAGTGAG
AAGGCTGGTTTGGAGTGTTTCAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTCCC

FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG
CAGTCCCGGACCAAGAGAGGGCGCGTGTTCCTCTTCGAGCAGATTGTCATCTTCAGTGAA
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAGGAGCATCAAGATGAAT
TACTTGGTCCTGGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACTCATGAACAGA
GAGACTTCTGAGAGGGTTGTTCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTTGAATGCACTGCAATCGCCC
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT
CCCCAAGCCAGCCCCAGGCCCTACTCCTCTGTTCCCTGCGGGCTCAGAGAAGCCCCCAAAG
GGCTCCAGCTATAACCCACCTCTGCCTCCCCTGAAGATATCTACCTCCAATGGCAGTCCA
GGGTTTGAATACCACCAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCTCGCCGTCAACCAGCAGAACATGTGT
CTGGTGTACCAGCCTGCCAGCGACCATTCCTCCCGCCGCGAGGGCTGGGTCCCAGGCAGC
ATCCTGGCGCCCCCTACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG
TCATGTTTCATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGAGAAACACGGGTAAA
AATGAAGCCACAGGGCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTATAA
GAGACGAACAGTTCAGAGGAATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG
ATCTTAAATCCAAATTCATCCAAGAAGTGGCCCCAGAATTCCTTGTGCCCTTGGTGGAT
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAAG
CCCACCATCACTTGGAAGGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC
ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCTGAAGATCTGTAATCTGATG
CCCCAAGACAGTGGGATTTATACCTGCATAGCAACAAATGACCACGGGACCACATCAACG
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCCAGGAG
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAACTGCACT
ATTTCTGGTTTACACTGTGGAGTACAGAGAGGAAGGTTCTCAGATCTGGCAGCAGTCAGTG
GCTTCGACCTTGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGTGTCTTATCAG
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCAGCGAGCCCTCGGAGTTT
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCATTTCTTGGAAGGAAAT
TTTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCCGTTTCTCTATAGTAAAG
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTAAACAAAAAATG
AAGAAGAAAGAACAGGCTGCCCACGAGGCTGCCCTGCTTCAGCACCTACAGCACCCCCAG
TACATCACTCTCCATGACACCTATGAGTCCCCCACATCCTACATCCTGATCTTGGAAGT
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAAA
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACAACTGCAGGGTT
GCACATTTGGACATAAAGCCTGAAAACCTGCTCATTGACCTACGGATTCCAGTGCCTCGA
GTGAAGCTCATTGACTTGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTACCAC
CTGCTGGGGAACCCCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTCATGCTGAGTGGGGTCTCCCC
TTCTTGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTAGCTTC
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTTCATCAATGTGATCTTA
CAGGAAGATTTTCGGAGGCGGCCACAGCAGCCACATGCTTGCCAGCATCCATGGCTGCAG
CCCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCCTAGCATGCTTCATA
GAACGTCGCAAGCACCAGAATGATGTGCGGCCTATCCCCAATGTCAAGAGCTACATTGTC
AACCGGGTGAACCAAGGGACGTAG

SEQ ID NO: 45_5R72_8_2_H

CGCCGCTGTTTTGTCTCGCGCGGCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA
AAGTTTCTCCCGGTGCAGAATTCGGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT
GTCGGAGACCCGCCAGTCCGCCGGCCCCGGCTTTGTTCTGTCGGAACTGTAGTGGTGAGA

FIGURE 2KK

AAAACCTCCATGCTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC
TGGGCTGTACAGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAGTTC
GAAATTACAGTTTTTCACCATCAACTACCTTATCCTTTTTTGGCCTGGTTTTCTTCCTCAAA
CAGTGGAAACATTTTTTAAAGTTGCTTTTGTGTCAGAGTTAAACAAATGGCTGATAGTGGC
TTAGATAAAAAATCCACAAAATGCCCCGACTGTTTCATCTGCTTCTCAGAAAGATGTACTT
TGTGTATGTTCCAGCAAAACAAGGGTTCCTCCAGTTTTTGGTGGTGGAAATGTCACAGACA
TCAAGCATTGGTAGTGCAGAATCTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA
GCATCTCAGCAACAATGGGGTCGGGGCAACTTTACAGAAGGAAAAGTTCTTCACATAAGG
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTGGAAGAATATTGGGAAAAGGG
AGCTTTGGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTA
AAAGTGAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC
ATTCTGAAAAGTGTAAAACATGAACACATCATACTGGAACAAGTATTTGAAACGCCA
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAACTCAAAGAAATCTGGAT
AGGAAAGGGCATTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAATATAATG
GTTAAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG
ACTCCTATCTATATGGCCCCCTGAAGTTATCAGTGCCACGACTATAGCCAGCAGTGTGAC
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCTTTTGGCA
AGCTCAGAAGCGAAGCTTTTGTAGTTAATAAGAAAAGGAGAACTACATTTTGAAAATGCA
GTCTGGAATTCATAAGTGACTGTGCTAAAAGTGTTTTGAAACAACCTTATGAAAGTAGAT
CCTGCTCACAGAATCACAGCTAAGGAACTACTAGATAACCAGTGGTTAACAGGCAATAAA
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAATAACCCA
GAAAGTGTGAGGAAAACACAACAGAAGAGAAGAATAAGCCGTCCACTGAAGAAAAGTTG
AAAAGTTACCAACCCTGGGGAAATGTCCCTGAGACCAATTACACTTCAGATGAAGAGGAG
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCTGCAACCAGTAAGGACAACCTTGAT
ATGTGCAGTTCAAGTTTTCATCTAGCAAACCTCCTCCAGCTGAAATCAAGGGAGAAATG
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC
GCCCTGTCCAGAACCAAAAAGAACTCTAAGGTTCCCTCCAGTGTGAGACAGTACAAAAA
CAAAGCTGCTCTTGTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG
CTGAGCTTGTAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTTGACCAGCTTAAAT
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAAGGACAGCCACCAG
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTTACTTCAAATTCT
TATGTTTAGGCACAGCTATTTATAGGGGAAAACAAGAGGCCAAATATAGTAATGGAGGTG
CCAAATAATTATGTGCACTTTGCACTAGAAGACTTTGTTAGAAAATTACTAATAAACTTG
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTCACATGTGTTTCGTGAGATTTTAGGTT
GCTATAGATTGTTTAAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAAGT
CTTGCCATTAACTTGCTGCTAAATTCCCAATGTATTGATTAAATCAATAAAAAACAGATG
TTACTC

SEQ ID NO: 46_SGK309_H

GGGTCCGCAGCCCCGCCCTCACAGGCCCTCCTCACTCCCCTAGGTAGATGGCCCCCTCAGG
GCAGGCCCCGGCGGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCGCCCTT
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCCTGCCGCCAACTAC
GTGGTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGGCTTTGGTGAGATC
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCCAG
CAGCCCAAGCAGGTCCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTCCGGC
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGAAGGAC

FIGURE 2LL

CATGTGTGCAGGTTTCATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG
AGCACCACATTGCGGCTGGGCAAGCAGATCTTGGAGTCCATCGAGGCCATCCACTCTGTG
GGCTTCCTGCACCGTGACATCAAGCCTTCAAACCTTTGCCATGGGCAGGCTGCCCTCCACC
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG
GATGTGCGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTCGCTATGCCTCAGTC
AATGCCCAACAAGAACCGGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG
CTGGTGGAGTTTGCAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA
GGGATGATCAAGGAGAAGTATGAGCACCGGATGCTGCTGAAGCACATGCCGTCAGAGTTC
CACCTCTTCCTGGACCACATTGCCAGCCTCGACTACTTCACCAAGCCCGACTACCAGTTG
ATCATGTGCTAGTGTGAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT
GACTGGGAGAAGGCAGGCACCGATGCCCTCCTGTCCACGAGCACCTCTACCCCGCCCCCA
GCAGAACACCCGGCAGACGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCCTGG
GGACCTGCTCCGGGAGAACACCCGCGGATGTGCTACAGGGAGAGCACCTGAGTGACCAGGA
GAATGCACCCCCAATTCTGCCCGGGAGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT
TGTCCCCCACCCCGGGGGTCTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA
CAAACCTCCGGATCAACATCGGCAAAGTAACTGCCGCCAGGGCGAAGGGCGTGGGTGGCCT
TTTCTCTCACCCCGATTCCCAGCCTTGTGCCCTGCCCTGTTCTCTCTAAGCACCTGT
CCCCCGCAATCTCCCTGCTTGCCCGGCCTCTGTTTCCGGTCCCTCCCCGGCACTAGCC
TCGCTGTGTCTTCCATCATCATCCTCTGTCTCCTTCACACTGAGGAGACCATCCGCC

SEQ ID NO: 47_AA234451_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAACAGCAGC
AGCAGCCGCGCGCGCCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCGCCGAGTCGGCGGTGGGGGATGGGCAGGCA
GTGGCGGTCCCGCCTGCCGAGGGTTAACCCCGCCGGTCCCGGTCTGAGCTGGACCAGA
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCAGGTTAAATGGAAACCACCCTTGG
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA
GAGCAGCTGGATATCCTGAGTGTGGAATCCTAGTGAAAGAAAGATGGAAAGTGTGAGA
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGGACATGCTCACCAGGGAA
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT
GCTGTTTTGAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTTATTGGCTGTGGGAGG
AATGATCGATTCAACTATGTGGTCATGCAGTTGCAGGGTCGGAATCTGGCAGATCTTCGC
CGTAGCCAGTCCCGAGGCACATTACCATTAGTACCACTCTCCGGCTGGGTAGACAGATT
TTGGAGTCTATTGAAAGCATTCAATTCTGTGGGATCTTGNCATCGAGACATCAAACCGTCG
AACTTCGCTATGGGTCGCTTTCCTAGTACATGTAGGAAATGTTACATGCTTGATTTTGGC
TTGGCTCGACAATTTACCAATTCCTGTGGTGACGTGAGACCACCTCGAGCTGTGGCAGGT
TTTCGAGGGACAGTTCGTTATGCATCAATCAACGCACATCGGAACAGGGAAATGGGAAGA
CATGATGACCTTTGGTCCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCCC
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAGGAGAGATATGACCACAGG
CTCATGTTGAAACATCTCCCTCCAGAATTCAGCATCTTTCTAGACCATATCTCTTCTTTG
GATTATTTTACAAAACCAGACTACCAGCTTCTTACATCCGTGTTTGACAAATAGCATCAAG
ACTTTTGGAGTAATTGAGAGTGACCCCTTTTGAAGTGGGAGAACTGGAAATGATGGCTCC
CTAACAACCACCACTACTTCTACCAACCCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAAATACAGATGAG
GTATTTCCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA
GATAAATTGCCTGGATCTCTGGGACACCCCGTCCCCAGGAGAAGGATGTTTGGGAAGAG
ATGGATGCCAACAAAAACAAGATAAAGCTTGGAAATTTGTAAGGCTGCTACTGAAGAGGAG
AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTGGGTACCAATTCGT

FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCACTGGTGCGAAAGTTACGTTCC
ATTACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG
TTCCTTGAGACCTGGTATAAAATAGTGTATTTTTCTTTTTAAAGCTTCTAAGGTACCATT
ATTATTGTTGTCATTGTTGTTATTATTATTGTATATTTCTGTTACATAAAGTCTTTCAAA
TAAGAAATCCTTGCAATTTTGTAACTGAGTCTATTCAGCTCCAATTTTCATCCATGTT
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCTAACACTAGGTACAAGTTAAATGAACAT
TTTTACAGTAACCTTTGTTTAGAAAGTAATCTCTTCCACACAACAGTGTAGTGCTGGAGAG
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT
AATTCATACACAAGGGACGGTGAGTTCAATTCACCTTTAGTGAAGACCCTCTAGGAGTAAG
ATACTGTGGGAAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG
TGCATGGTTTTGAGGCACATTATCCCTACAACAAATTTTGATAACAGAAGAC

SEQ ID NO: 48_AA435956_H

ACTTTTACTATATTCTTTGAGATGACTGTTTTGATTTAGAGGCGAAATCAGCACGTGGT
GGCTCAAATCTCCTTATGGATAGTGTTTTCTTCCCTCCAGCTTTTCATGTTTCAACTTTTG
CGGGGCTGGCGTACATCCACCACCAACACGTTCTTCACAGGGACCTGAAACCTCAGAAC
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCCGGGCCAAG
TCCATTCCCAGCCAGACATACTCTTCAGAAGTCGTGACCCTCTGGTACCGCCCCCTGAT
GCTTTGCTGGGAGCCACTGAATATTCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC
TTTATTGAAATGTTCCAGGTCACCTTTGTTTCTGGGGTTTCCAACATCCTTGAACAG
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC
AAGCTACCTAACTACAATCCAGAATGGTTCCCACTGCCTACGCCTCGAAGCCTTCATGTT
GTCTGGAACAGGCTGGGCAGGTTCTGAAAGCTGAAGACCTGGCCTCCAGATGCTAAAA
GGCTTTCCCAGAGACCGCGTCTCCGCCCAGGAAGCACTTGTTTCATGATTATTTTCAGCGCC
CTGCCATCTCAGCTGTACCAGCTTCTGATGAGGAGTCTTTGTTTACAGTTTTCAGGAGTG
AGGCTAAAGCCAGAAATGTGTGACCTTTTGGCCTCCTACCAGAAAGGTCACCACCCAGCC
CAGTTTAGCAAATGCTGGTGAAAAGAAAGGGCGAGATCACCAAGGTTCTTCCAGGGCTGT
ATTTCTGCAGTTTTCGGTTTTCATTTGCTTCAGCTTACTAAGAAGCTTCAAATCTAACTCC
ATACTGAACAAGGGGCTTTATGTCCTCACCTATGACCTGGAATAGTTTAAATATGGTGTT
CAAGGCAATAGTACATAATAGTGGAAGAAAATTCAGTGGAAGGTTATTGCTATTGTCAAT
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAACTAAGTCTAAGAAG

SEQ ID NO: 49_AA626859_H

AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA
TTTCTGTCATATACATAACTGTATTACAGAGATATAAAACCTGAAAATATTCTAATAAC
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA
TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGA
TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCT
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA
TGGCATCAGTATACCTGAGCCAGAAGACATGGAACCTTTGAGGAAAAGTTCTCAGATGT
TCATCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTCAAGAGGCCCAAATTAA
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAACAAGTCCTCCAGTTAA
ATTTGATCACCTTCCAAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT
GTACACATTTTGTACAAGTGAGATAGGAATTCAGTGTTTCAAATGCAAATGAGCCATA

FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGGCTCTGATCATTGCTGATTCCCTTTCCCCA
TGCTTTTACAT

SEQ ID NO: 50_AA061797_M

GAAAATAGCCCTGCGGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT
CATCGAGGTGTTTCTAGAAGAAAGAGAAAGATGCATCTAGTTTTTGTAGTACTGTGATCACAC
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAGTGT
GCTATGGCAAACCTTCAAGCCCTTAACTTCTGTCAAGCACAATTGTATTTCATCGGGA
TGTAACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG
ATTTGCACGAATTCTAATTCCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA
CCGAGCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGC
CGTCGGCTGTGTTTTTGCAGAGCTCCTGACGGGTGAGCCACTCTGGCCGGGAAAATCCGA
CGTGGACCAGCTTTACCTGATCATCAGGACGTTGGGGAAGCTGATTCCAAGACACCAGTC
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA
GACTCTTGAAGAAAAATTCTCAAATGTTTCAAGCTGTGGCTTTAAGTTTCATGAAGGGATG
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCAGCTGCTGGACAGTGCCTACTT
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAAGCCGAAG
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCCTGGAAGCCACATCTCCCCACACCTGA
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTCGATCATCTTCCAAACATTTAGGGGACTCA
TCCTTCCCAGCACATCCTTTTAAATATTGCTACATAGGAATAAGACGGGAATCCTCAGCA
TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC
CTGTGCTTTTTTCCACGCCAGCTCCATCTCCTAAACATTCTCTTTAAATGTTGCAGTATC
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTACCAGAGCCGGGCTTCTCAGGCAA
TCGGTACTGTGCATCTGTGGACTTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT
CTCACTTCAGCCGACCAGTGGTGTCTGAGCAGACCCAGATCTGCTGGCTGCTGTTGT
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT
TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA
CGAACTAGAGAAAATTCCAAACGTGACCAAGTTAGTGGACAGACTACAAGGAATCGACCAC
CATACCACAGTAACGCCCCCTGGATCCCTGGCTGCCACCCACTCTAAGGCTATCCTGGTT
CACCATGGTTTTCTCTTTCTTTCTTTTCTTTTAAATCTATTTGTACATATGAGAAAGAGGC
AGAGGGGCGAGAGAAAACCTCGTGTGTGAAAATCAAAGACAAGCAGGAGGCCAGCCTAAG
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCAAGTCCCT
GCTGCTGATTGTATAAACTATGAATAAGTCTACATATGTAGGACATATTGTTGTCTATTG
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTCTAAATATTCTCCACACTGGTG
AGTATCTTGGCATTTCATTTCTGACCTCATCACAGATGAACACATCAAAGGATGAGTATG
TATCACTTTGCATCTTAGAATTCTACCTGTTTTAGCTGCGTTAAACCTTGTGAAAGGGCG
GGGCCATAACTGAACCTGTGGAGTTCTTGCTGTGTGCAGGAAACCTCTGGTTTTGTCT
CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAATTCAAAGTCACT
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG
TCCGTGTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC
ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAACCTAATAGGAGTCGTTGAAGGTAG
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTAGTTTAGAAT
GCATTAATGTATGTAGAAGCTGGGCTATTTAGATTATTTGAAATTGTAGCTATTGTTAA
TTAGCACTTAATACTAACTAGCATTATGGTAGTCTAACTATTAGAGTTTACTACAAAG
AGGTTTTGATTGAATTATATTAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA
GAAAGCTATATAAAGATTAAACATTTTTGTGGCTGTATATTTGTGTATATACCTTGGTTG
TTCTTTAAATTATTTTAAATAAAAGCCAGAAACATT

FIGURE 200

SEQ ID NO: 51_AA397553_H

ATGCCCAATTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAAC
TTGCAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG
AAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCGAAGCA
GCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGT
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGG
GACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAGCCAAGAAGTCTCCAGCAAGTCG
GGATCGATGAAGGACCGGATATCGGGAAGTTCAAAGCGTTTGAATGAGGAGACTGATGAC
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCATCCAAGCTCCAC
AAGGAGAAGACCAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAGT
CATCGAAAAAGGGAAACACCCAAAAGTTACAAAACAGTGGACAGCCAAAAACGGAGATCC
AGGAGCCCCACAGGAAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCCTCGGGAGCT
TCTTATGGCCAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC
TCCTACAAGAAAAGTCTTGGAAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG
GAGCCTTCGGCCTACCACTCCAGCACCCCGTCCAGGAGCCCCCTACAGTAGGCGACAGAGA
TCTGTCACTCCCTATAGCAGGAGACGGTCGTCCAGCTACGAAAGAAGTGGCTCTTACAGC
GGGCGATCGCCAGTCCCTATGGTCAAGGCGGTCCAGCAGCCCTTTCCTGAGCAAGCGG
TCTCTGAGTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCTT
GCATATTCAAGACATTCATCTTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGT
CATTCAGTATCTCACCTGTCAAGCTTCCACTTAATTCAGTCTGGGAGCTGAACTCAGT
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCC
AAGGGTTCACCTGTATTTTTGCCTAGAAAAGAGAAACAGTTCAGTAGAGGCTAAGGATTCA
GGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAATAATTGGAAAAATCTGCCCCAGATACT
GAACTGGTGAATGTAAACACATCTAAACACAGAGGTAAAAAATTCTTCAGATACAGGGAAA
GTAAAGTTGGATGAGAACTCCGAGAAGCATCTTGTTAAAGATTTGAAAGCACAGGGAAACA
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAGGAGACAGAAACA
TCAGAAAAGGAGACCCCTCCACCTCTTCCACAATTGCTTCTCCCCACCCCTCTACCA
ACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCCTCCAATACCACTCTT
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCTCTGCTTCCAGT
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGTCTCTCAGGCAAT
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAACAGCTGCTATTCCA
CACCTGAAAACCTTCAACGTTGCCTCCTTTGCCCTCCCACCCTTATTACCTGGAGGTGAT
GACATGGATAGTCCAAAAGAACTCTTCTTCAAACCTGTGAAGAAAGAGAAGGAACAG
AGGACACGTCACTTACTCACAGACCTTCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTG
TCTCCCCCAGACTCTCCAGAACCAAAGGCAATCACACCACCTCAGCAACCATATAAAAAG
AGACCAAAAATTTGTTGTCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGG
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA
GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTTCGTGAAATCAAAATCCTTCGTGAG
TTAATCCACCGAAGTGTGTTAACATGAAGGAAATTGTACAGATAAAACAAGATGCACTG
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGATTTGAGTATATGGACCATGACTTA
ATGGGACTGCTAGAACTGGTTTGGTGCACTTTTCTGAGGACCATATCAAGTCGTTTCATG
AAACAGCTAATGGAAGGATTGGAATACTGTACAAAAAGAAATTTCTGCATCGGGATATT
AAGTGTCTTAACATTTTGTGTAATAACAGTGGGCAATCAAACCTAGCAGATTTTGGACTT
GCTCGGCTCTATAACTCTGAAGAGAGTCGCCCTTACACAAACAAAGTCATTACTTTGTGG
TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG
AGCTGTGGATGTATTCTTGGGGAATATTACAAAGAAGCCTATTTTCAAGCCAATCTG
GAACTGGCTCAGCTAGAATGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG
CCTGATGTTATCAAACCTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTTCATTCTCTTCTGCAGCACTTGATTTATTGGACCACATG
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT
AAAGATGTGGAAGTACAGCAAAATGGCTCCTCCAGACCTCCCCACTGGCAGGATTGCCAT
GAGTTGTGGAGTAAGAAACGGCGACGTGAGCGACAAAGTGGTGTGTAGTCGAAGAGCCA
CCTCCATCCAAAATTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG
AACAGCAGCCCAGCACCACTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAAGCCCTGAACCAATCCATCAGTGCCCTG
ACGGAAGCTACTTCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG
GAAGCACCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCTTGAAGCTTCA
AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG
CCCCGAAGAACTCCCAATGCCACAGGAGGAGGCAGCAGCATGTCCTCCTCACATTCTT
CCACCAGAGAAGAGGCCCCCTGAGCCCCCGGACCTCCACCGCCGCCACCTCCACCCCCCT
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC
TTGCTGCAACTTTTATCCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC
ACTGATGGGCCTGAAACAGGGTTTCACTGCCATTGACACTGATGAACGAAACTCTGGTCCA
GCCTTGACAGAATCCTTGGTCCAGACCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCACTGCAGTTTCCAGGGGAC
CAGGACCTCCGTTTTTGCCAGGGTCCCCCTTAGCGTTACACCCGGTGGTGGGGCAACCATTC
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAATTGCAAAACTAT
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG
GGCCCAACTCAGTCTTCTGCTTATGGAAAACCTATCGGGGGCCTACAAGAGTCCCACCA
AGAGGGGGAAGAGGGAGAGGAGTTCTTTACTAA

SEQ ID NO: 52_AA789239_H

TGAAATGGAGATGTATGAAACCCCTTGGAAGAGTGGGAGAGGGAAGTTACGGAACAGTCA
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAAGATATTTTATGAGAGAC
CAGAACAATCTGTCAACAAAATTGCGATGAGAGAAATAAGTTTCTAAAGCAATTTTCATC
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAGAAAATTCAATTTGGTAT
TTGAATTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTGATGGACTAGAGA
GTAAGCGACTTAGAAAATACCTCTTCCAGATCCTTCGAGCAATTGACTATCTTCACAGTA
ATAATGTAATCATTCATCGAGATATAAAACCTGAGAATATTTTAGTATCCCAGTCAGGAA
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAGATACTTCTT
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA
CTGGAAATCCCTATCTTCTAGTAGTTCTGATTGGATTTACTCCATAAAATTGTTTTGA
AAGTGNGATTGATGCCAGAACTGAAAGCTAAATTACTGCAGGAAGCAAAAGTCAATTCAT
TAATAAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAACAG
TTTATACCAATACACTGCTAAGTAGTTCACTTTTGGGAAAGGAAATAGAAAAAGAGAAAA
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAAGTCAAAGGAGGAAGAGGAGATATCTCAG
AACCAAAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAAATGAAAATGTTC
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATGTAACCACCAAAACCTATCAATCCCA
GCACTAACTGTAATGGCTTGAAAGAAAATCCACATTGCGGAGGTCTGTGACAATGCCAC
CCATCAATCTAACTAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTCACC
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAGAGACGCACTTCTTCACAATCTATTGGAC
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCTTATCAAAGCCAAATGGAGAAGG
GTATATTTAATGAGCGAACAGGTCACAGTGACCAATGGCAAATGAGAACAAAAGGAAGC

FIGURE 2QQ

TGAATTTTCCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC
AAGAGTTTATTCCTTATCTCTGCTGTCTGCCTGCTGTCCTATTTTCACAAATATTTGCT
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG
GTTTTTTTTCTGGTAGTGTCTTTTCTTTTACATAGTCCAAAAAATACAAGATGACAACCTC
TTCCCGTTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC
ATGTGCATGAGCATCATCCAGCTTTTTTTGTTAGCAAAACATTTACTGTTTTCTTTTCCC
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC
CTTGAA

SEQ ID NO: 53_AA124976_M

CTGGCAGATATAGTTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT
GATCTTTTGCCTCACGATTACTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCAGACCAGAAGAAGCCA
GAGTATGAAGGCGACCAACCGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCCAGTGAGAATTCTGAC
GGTGTCAAAGAAGACCCACACGCTGGGGGTTGTATGATAATGCCACCTATCAACCTGACA
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCCACCCCAATTCACGGTTA
ACTGAAAGAACAACAAAAGAGACGCACTTCTTCACAACTATTGGACAGACTTTGTCTAAT
AGCAGACAAGAGGACACAGGTCCCAACAAGTCCAAACAGAGAAAGGTGCATTTAATGAG
CGAACAGGTGAGAATGACCAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA
TGCGACAGGAAAGAATTCCATTTCCCTGAACTGCCATTACAGTGCAGGCGAAGGAGATG
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTTCCCGATAGTGCTTT
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTTATTTTATATAC
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT
CTATTTTTTTGGTTTTGCTAGCAAAATTTTACAAATTTTTCTCTATCTTCCAAAACTGT
TATTTTGATGCTGTGATTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCATGATGAAAGA
CATTCTATTGTCCCAGTGAAGCATTATAGTACTTACATAACATGTTACAGTGATATGA
TGTTCTAGGTTAAACTCCTTGAGATGAAACTATTTCTGCAATCTCTGACTCCCCTAGT
CTAATAGTTCCCTTCATTTAGCCAGAAGAATTTCTGGAAGAAGCGATGCACAACCTGGGA
AAGGTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA
GTTAACAT

SEQ ID NO: 54_AA575635_M CCRK_M

AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCCGGGTCTTCTCTCCGGAT
GGTGGTCGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACCTCTG
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACTGTGCTGT
GTGCTTCGCATCCTGGGTACCCGAGTCTCGAGTCTGGCCGAGATCACAGAGCTGCCT
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAAGTGGCCCTGGAGGAGGTGCTGCCT
GATGCCTCTCCCAGGCCTTGGACCTGCTGGGCCAGTTCTCCTCTACCCCTCCACGACAG

7/113

FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTTCACAGCGCCTCTGCCTGCC
CATCCATCCGAGCTGCCAATTCTCTCAGCGCCCAGGGGACCTGCACCCAAGGCTCACCCA
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC
CCAGAACTGATTCGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCTTCCTGCT
CGCCCTAGGAGCACCTCTTTCTGATTTGCCTCCATGGCCTCCCCACGGCTATATATACCA
CACCTGGTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA
TGTTTCATCCCAGCAGAGAAAGAGACTCACGTCTACAGACAAAGCCTCCAGAACTGCTA
GCTGTGTCCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC
AGGCTCTGTCCCCTCTTCAAGGACATTGGTACTACAGCACCACCTGGTGGAAGCACAGAG
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT
CCACTGGGTCCAGGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTCTGTCTAATTGCACC
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTCACAGGGGTCAAGTACT
CAGAAGGGGCCCTCCTGTGAAGGCCATTTGGGTCTCAGGCTTCCCATGCTATTCACGGGA
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCAGGGATGGACAGTCCAG
TTCCCGAAGCCCACTTCCACATGTCGGGTGGGTCACTCAGTGAGCCTGAGGCTGCCTTG
CAGATGCGGAAGCAGGCATTCTTGAATCCACTCAGTAAATAAATTCAGTGTGACTCAG

SEQ ID NO: 55_AA631990_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA
TCTGGTCACACTCACTATCCATTTCATGATTACAACCTCTTCAATACTATCGCGGCCGAGGA
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG
CGGCATTCCAAAAGAACTCACTGTCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTCTATTATTTAGAAGCAAGGTCC
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT
GAAGGATATGTTCTTAGACATTATCAGAGACATTGAAAGCGGGTATCGAATCCACTGC
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGT
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGGACACTTTGGGTGAAGGAGCCTTTGGC
AAAGTTGTAGAGTGCATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAAATCGTA
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTA
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT
CATGGTCATGTTTGTATTGTGTTTGAAGTACTGGGACTTAGTACTTACGATTTTCATTAA
GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAA
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
CTTGGTTTTCACAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
ATATTAGGACCCATACCACAACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCAC
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC
AAACCGTTGAAGGAATTTATGCTTTGTTCATGATGAAGAACATGAGAACTGTTTGACCTG
GTTTGAAGAATGTTAGAATATGATCCAACCTCAAAGAATTACCTTGGATGAAGCATTGCAG
CATCCTTTCTTTGACTTATTAAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA
CTTCTCTAGAAGAGATTACTTAAGACTGTGTCACTCAACTAAACATTCTAATATTTTTGT
AAACATTAAATTATTTTGTACAGTTAAGTGTAATATTGTATGTTTTGTATCAATAGCAT
AATTAACCTTGTGAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAATAATTTT
TCTTTTGAATTAACCATTTTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT
GTGATTGATCTTGCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTTTGAGTAA
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

FIGURE 2SS

ACTTAACTTTAAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAAGTCTAG
ATAAGCAGGTACTAGAAACCAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAAT
TTAAGTGTGTATTCTTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAAACCATACACACTTTATTT
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT
GAGTCACAGATATAAAAATAGAAATCTGATGAGAGTTTCAGTTTTTAATACCAAGTCC
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAAATACGTAAACCTAT
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA
TTGGTTACATAAACTTTTTGACTTCAAT

SEQ ID NO: 56_AA557536_H

AGTAAGGCCCCGCGGGCGTCTGCGCCCATGTGCACCGTAGTGGACCCTCGCATTGTCC
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCCTCTGGCCTTCCAGCC
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTTTGAGTTTATGGACACTGACC
TGAACGCAGTCATCCGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT
ACCAGCTCCTGCGGGCCACCCGGTTCCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCTGAGGACCAGGCCGTGACAGAGTACGTGG
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTTCGCACCGCTACACCGCTCCT
GCCCCAGATACACCCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC
TGCGGGGGAGACCCCTGTTCCCCCGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG
AGACCATCCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC
CGCCAGACACCTCCCCAGAGGCCCTTGACCTCCTTAGGCGACTCCTGGTGTTTCGCCCCGG
ACAAGCGGTTAAGCGCGACCCAGGCACCTGCAGCACCCCTACGTGCAGAGGTTCCACTGCC
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCCGGGCACACGAAGGGGTCCAGC
TCTCTGTGCTGAGTACCGCAGCCGCTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA
GCGGCACCTCGAGAGAGAAGGGCCCCGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA
AACCCAGAGCCGACCCCTCAGCTGCCCTTAGGACACCTGTGCAGGGTCCCAGACCCAGGC
CCCAGAGCAGCCCAGGCCATGACCCCTGCCGAGCACGAGTCCCCCGTGCAGCCAAGAAGC
TTCCAGGCAGAACTCCGCTCCCCCTGCTCCAACTGCTCTCCTAGGGAATGGGGAAAGGC
CCCCTGGGGCGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG
GAGCTGCGCCCTCCCTGACCTCCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC
GGGGTGACTGGAACCGGGGCGGTGGGGTGAGGGTGGCCAGCGTACAACAGGTCCCTCCCC
GGCTTCTCCGGAGGCCCCGGCCCCGGCGGAGGATGTTACGACCTCTGCCTTGACGGGTG
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC
ACTCGGCACTGGGCCACCTGCCCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC
CTTACCTTGCCCTCTGTTCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCCGTGAAGTTCAGGGAGCTTGCCCCGGGT
CTCCTCGGGGGAGCAGATGAGGGCCCTGCCC

SEQ ID NO: 57_N28606_H, MOK_H

ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAACGTTTTCTGAAGTTATGAAG
ATGCAAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAA
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGGACAGAAAATCTGGTTCTCTTGCACTA
ATATGTGAACCTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA

FIGURE 2TT

TCAGAAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTAC
AGAAATGGAATATTTACAGAGATGTAAAACCAGAAAATATACTAATAAAGCAGGATGTC
CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCC
CTCTTTTCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTCATCGGCACA
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCTT
TTTAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCACCAGGCCCTG
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA
AAAGCTGGCTTTCCGGAGCACCTGTGGCACCGGAACCACTCAGTAACAGCTGCCAGATT
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA
CGAGGACCGGCCTATGTCATGGAAGTGCCTAAAGCTTTCTGGGAGTGGTCAGACTG
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG
CCGGTGCTGAGACCCCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCCGCAGAAGGAC
CTTAAGCCTGCCCCGCAGCAGTGTGCTGCTGCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58_AB023153_H, ICK_H

ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCTGCTG
GGAAGAAGCATTGAGTCTGGGGAGCTGATCGCTATTAAAAAATGAAAAGAAAATTTTAT
TCCTGGGAGGAATGCATGAACCAACGGGAGGTAAAGTCTTTAAAGAAGCTCAACCATGCC
AATGTAGTCAAATTTAAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG
TACATGAAGGAAAATCTTTACCAGCTCATTAAAGAGAGAAAATAAGTTGTTTCTGAGTCT
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTCACAAACTCGGC
TTCTTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA
ATTGCAGACTTTGGTTTGGCCCCGAGAAATACGATCAAAAACCTCCATATACAGATTATGTA
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCCC
ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAAGTTTACACCCTCAGGCCACTCTTC
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAAA
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACTTCCGTGGCCACAG
TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACTTCGA
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCAACAAAACCTTCAGGATTCA
GAAAACACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAAGCCAGTC
CCACCTGCCAGCCACCAGCCAAGCCACACACACGAATTTCTTCACGACAGCATCAAGCC
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCGTTGCTTTTCCCATCCCTCCACAACAAG
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAAATGGTGAGATAAAGCCAAAG
AGTAGGAGAAGGTGGGTCTTATTTCCAGGTCAACAAAGGATTCAGATGATTGGGCTGAC
TTGGATGACTTGGATTTTCACTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA
CAGAGTGATGACACTCTCTGCAGGTTTGGAGTGTGTTTGGACCTGAAGCCCTCTGAGCCT
GTGGGCACAGGAAACAGTGCCCCCACCAGACGTCATATCAGCGGCGAGACACGCCCCACC
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCCTGGGATCAGT
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCACCTAATCCATGGTCT
AGTTCTGGCTTGTCTGGAAAATCTTCAGGGACAATGTGAGTAATCAGCAAAGTAAATTCA
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAAACTATGTCCCTTCTTTCTG
AAAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCCAGACCCTTCC
CCTGGTTATTCCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATCTTGGACACC
CAGCCTAGAAGCACTCCTGGGTTGATACACGGCCTCCAGCCGCCAGCCAGTGCATGGC
CGGACAGACTGGGCTTCCAAGTACCCATCCCGGCGGTGA

FIGURE 2UU

SEQ ID NO: 59_AA839940_M

AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG
CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCAG
GGCCCAGGAAGAACTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTTGAACACCGGGTAGTGAGCATCAAAGAT
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTTCGGTTT
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG
CTCAGCCACGTAAACTTGATCCAACCTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTTGACCGGATCACGGATGAGAAGTAC
CACCTCACTGAGTTGGATGTGGTCTTGTTTACGAGGCAGATCTGTGAGGGTGTGCATTAC
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTCAGC
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATACAAGCCTCGG
GAGAAGCTAAAGGTGAACCTTTGGTACTCCGGAGTTTCTGGCCCCAGAACTTGTAACTAT
GAGTTTGTGTCAATTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC
TGCAGCTGGGATTTTCGATGCTGATACCTTCAAAGGGCTGTTCGGAGGAAGCCAAGGACTTT
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTTCGCTCAGATCC
CAACAACTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC
CACTGGGCCTGGGAATTCCTTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAATGATGGA
AGGAAGCAAGAAAAGAAAAGAAAAGAAAAGGGGGAAGAAAAGGAAAAGGCAGAAAAGCAA
GGAAAAGAGGCTACGTTGTTGCTCTTCTGTAGGTGAAAGTGTTTTTATTAAAAGCCCTAG
GAATGTTTTTCTGCCTCGTAAGGTCAGCAGGTCTCATATGCTGCTTGCTACCCCCGACCC
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCCTACTTGGCTTT
TGGTCAAATTTGAATTCTAACTTGTCTATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA
TTCTTAAAGAATTAATAAAATATATTTTTTAAAGGAG

SEQ ID NO: 60_AA460132_H

GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAG
TGTCCGGGGTGGACGCATTCGGGTAGCCGAAGAAGTCCAGGATTGCCGAAGAAGTCCCA
GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTACAGAGACAGCTGATCGGTTGGAG
CTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACGCCGGCCGATGGCGAGGAG
CCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCGGGAGCGGAGCAGCCGCTTCTTGAGC
GGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCTGTTCCGTGGCCGCTTCCAGGGC
CGCGCGCGGTGATCAAGCACCGCTTCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGCTCCTCCGTGTGCGCGCT
GGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCCAACCTGCTTATATATGGAA
GAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTAGTCCACTATGGAGACTGAAAAA
ACTCCCCAGGGTCTCTCCAACCTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC
GATGAAGACCTCATTGATGCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCATTTAGCACTTCCAGAG
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCTCAGTACCCATCCCAACACT
GAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAGGCCAGGCCA
GTGCTAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG
AGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAAA

FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTTAAGTGGTATGTG
ATCGTGTCTATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCCAGATTGTGACATGTA
TATCTCAGATACATGGGTGTGGCATTGAACACATAATGAGAACATTATTCTCTTTTTAG
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT
AACCCAGTGTTTTTTTTTTGTGTTGTTGTTGTGTACATGTTATATTTATTTTGAAACCAGTTT
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61_SGK034_H

CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG
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CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC
ATCTTCATCACAGAGTACGTGTCTCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG
AAGAACCACAAGGCCATGAACGCCCCGGGCTGGAAGCGCTGGTGCACGCAGATCCTGTCT
GCGCTCAGCTTCTTGACGCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC
ACCATCTTCATTACAGCACACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC
TCCAATGCACCTTCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACTTCGG
AACCTGCACCTTCTTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC
ACCCGGGTACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG
CGGGAGTTCATCCTTTGCTGCCTGGCCCCGGGACCCTGCCCGCCGGCCCTCTGCCACAGC
CTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC
TTCATCCAGCACAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGAGGCCCGCTGCAGTGGCGG
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTCAGGAATGGAATC
TACCCACTGATGAACCTTTGCAGCCACTCGACCCCTGGGGCTGCCCGTGTGCTGGCCCCA
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC
AGAAAGGTCTATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT
CTCACTCTGCTTCTGGTGTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC
CCAACGGACAGCGCCAGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCTCTCCACGAG
GACGACCGGATGAAGCTGGCCGCTTCTCTGGAGAGCACCTTCTCAAGTACCGTGGGACC
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGCTGCCCGGGCAGGCC
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAAG
GCCCCGGTAGTGAAGGAACCCCCCTCTCTGAGAGTGGGGCTGACCCTGCCTTGGGCGC
CGAGGGGTGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCAGGTCCTTAGGATCAGG
GTTGCCCCCAGAACCCCTTCCCATATCTCCATTCTCCGCCCTGAGTTCCTACCCAGGCT
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCAGC
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCAGGGAACTGCTCCAT
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC
AGCAAGCCAGCGGTGACACACCTGCAGGTGTCAGGCATGGCACTGGGCACAACAGGGACC
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTGAGCAAAGCCCT
GGTCCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCCTGAGACCAG
AAGTTGCAGCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCTCCAATGGGCTTTTTTC
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC
TCACAGCCCCCTCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCTGGGCCT
CTGAGGATGTCAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCTGGCCTCTTGATTCTTGCTT
GCCTCTCCTCCAATTCCAACTTAGTGAAATGGCCTTAAGCATTTTAACTGTATGTATA
CATTAGCGCATTCATGCCTTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC

FIGURE 2WW

TGTATTAGTTTTATACTGCCGCTGTAAAATTTACCACAACTTAGTGACTTAACACAAAT
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC
TGGCAGGCTGCCCTTCCTTCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG
CTGCTGGCAGAAATCCACATCCTTTTCGGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC
TGTAACATAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCTTGGCTCTTGGCCCC
CTCCTCCATCTTCAGAGCTAGCAGGTTCACTGTGTGTACGAACCATTTCTCTGGTTCCC
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCCAGCCAGATAA
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT
GCCATGTAACTAACATTCACTGGTTCAGGGATTAAGGAATGAACCTCTTTTGTGGGG
AAGGGTGGCATTCTGCTGACCACAGCACTCCAACCAAAGGCCAAAACCAAAGCAAGACT
TACTAACGCATATCAAATAAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA
TTCCAATACTATTTACAAAATTATTCAAATTCTCACGCCTTCCAACCTAAAATTAGCAAT
CTAAAGTAATTTCCATATCCTAGATGGAAACCCTCATGCTAAACTGTCTGATTATGCATG
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AAGC

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CCACGCGTCCGCACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG
GGAATTCATCCTCTCCTGCCTGGCCCCGGGACCCTGCCCCGCCGACCCTCAGCCCACAACCT
CCTCTTCCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA
CCTCCATGCAGTTTTTGGCTGAGATGCCGCAGCCCCATGGACCCCAATGCAGTGGCGGTA
CTCAGAGGTCTCCTTCTTGGAGCTGGACAAATTCTAGAGGATGTCAGGAACGGGATCTA
TCCACTGATGAACTTTGCGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC
CCCAGAGGAAGCCCCAAAAGGCCAAAACCTCCAACGCCAGAACCCCTTTGACTCGGAGACCAG
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC
AACGGACAGTGCCAGGACCTCGCTGCTGAAGTAGTGATTATGGCTTCCTGCACGAGGA
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACTTTTCTCAAGTACCGAGGGACGCA
AGCGTGACCTTCCCAGTCTGACGGCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACCTGAAC
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCAGCTTTCTGCAGCAGTGTGGGACCCT
GGGGTGGTGATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTCAGTTAGGGGAACCG
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG
CCTGAACTCAGGTGTCACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCTTGGTCTGCTCA
GACCAGTCTGATCCCTTGACAGCTGCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT
GAGACCAGGACCTGTGTCCTCCCCAAAGCCCTTGGGAAGGATCTTTCTATTTCATCATCCC
TCTGGCCTAGGGGCTCAGGGGTGAGGCATCCTCCACATTCCCTCCCTGGGGAAGTTGTGT
GTTTGAGTTGAGGATGTGGGTTCTTGGCTCCCTCTTTCTCCCCAGCCCAACTTGTCTCTT
TCTTACTGGTTTCAAAGTCTGATGAACGCTTCCCTCAGAGCCACCCTGGTTTCTTGG
TTCTTGAAGTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTAAATGCATAT
ATAAATGTAATGCAGTCACGGTCTTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCCAGTGG
TTTGAGACGACACACACACACACACACACACACAGAGAGAGAGAGAGATTCTGTA
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCCTTTCTGGAAG
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCTCTCAGCTTCTAGAGG

FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT
CTTTGTCTCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCTTCTCAGGGTCTATAGATGAAC
CACACCTGCGCAGTTCCTTCTGCTGTTCATCCTGGGCTTTGGTGCTTGGAGAACAGCCGTG
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA
AATAAAACAGATTTGTCATGGGACATCTAATAAATTAAATGAACCTCTG

SEQ ID NO: 63_NEK7_H, N34132_H

CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGCGCCGCGAG
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ACGGCTCCAGCTCCGATTCCTCCGTGGGGGAGAACTGGGAGCCGCGGCGCCGCGACGCTG
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCGCCACACTATGGACAAGGACAGCCGTG
GGGCGGCGCGACCACTACCACCACTGAGCACCCTTCTTCCGCCGGAGCGTCATCTGCG
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCCCTTCTCTTCCCTGCCCCAGCCCAGCA
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG
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CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCCGCCGCGAGAAGTGGCAGCGGCG
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC
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AAGAAGCTGAAATGTTAAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCTCT
GGGAATCCACAGTAAAAGGAAAGAAGTGCAATTGTTTTGGTGACTGAACTTATGACGTCTG
GAACACTTAAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT
GGTGCCGTCAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG
GAGACCTCGGTCTGGCAACCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC
CAGAGTTCATGGCCCCCTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA
ATGCTGCGCAGATCTACCGTCGCGTGACCAGTGGGGTGAAGCCAGCCAGTTTTGACAAAG
TAGCAATTCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAAACAAAGATGAAA
GATATTCCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG
AAGATATTAAGAAATTAAAGGGAAATAACAAAGATAATGAAGCTATTGAGTTTGTTTTG
ATTTAGAGAGAGATGTCCCAGAAGATGTTGCACAAGAAATGGTAGAGTCTGGGTATGTCT
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAAACAAAAGCAGGAAGAGA
GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCCAGACAGGAATCAAGCAGCTCC
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG
TAGAACCTGAAGAACCTGAGGCAGATCAACATCAACAACCTACAGTACCAGCAACCCAGTA
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTCACAGAAT
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCCAANNCATGAACAGGCACATT
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG
GGGTATATCCACCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCCTCTCAACAGA
CAGTGCAGTATTCACCTTTCACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG
TGAGTCAGCCTCAAGCTCCACAAGTCTTGCCCTCAAGTATCAGCTGGAAAACAGAGTACTC
AGGGAGTCTCTCAGGTTGCTCCTGCAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTGAGATGTTGCTTCAGGTATGA
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

FIGURE 2ZZ

CTTTGTATACCAAAGTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC
TTTCAGGGAGAAGACGACGACCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT
CCTTGGGGAATAAAAGCCCCCAGCTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG
TCTTGACCCCCCAGCAGACCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC
AGCTGTTACAGCCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTACGCCTTCACCA
GTGATGGTGCCATTTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTTAAG
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACACTGAAGAATCTGG
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC
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TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATCCCACAGAG
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA
GATCAGTCTCTTCACAGGAAGAATGCACTTGATTGGTAAGGAGGGCAAAGTAGCTAGCAT
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT
CATCTCTTACATATCTGACCTTCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG
CATTTACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC
TCTCTGTGTTCTACCCTGTTTTTCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT
GGCTCTTTGTGTGTAACACCTTTACTCCTTCCTTGTCTTGTGTTTCTGCTGCTTGGATC
TGATGTTTTACGCAGTCCATTTTCAATTGTCTCTTTTTGTATATCATCTACTCAGTGGCT
TGGCTGAATTACTGTTACCCTCAGAAAGTTTGGGCCCCCACATTAATTATGATAAAAAATG
TCAAATAACAAGTTATCTACAAATTTCAATGTAACCTTTCTGGTAGAAGTGCTTCTTCAT
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCAATTTAGAAT
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA
GGCGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC
CCATCTCT

SEQ ID NO: 64_BCON3_H

GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT
GAAGCGCAGGCTGCGGGGCGCGGAGTCGGGAGGCCTGAGTGTTCTTCCAGCATGTGCGGA
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC
AGCTCCTGGCCTGACATCAGTGTACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC
AGAGGAAGAAGAAAGAAAGTGAAGATGAGTCTGAGATTTTGAAGAGTCGCCCTGTGGGCG
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA
ACGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTCTGTGCTGTGTTTGATAATCTGATTCA
ATTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAA
GGCCAGGGTCATTTTATCACAGAATACATGTCTGAGGAGTCTGAAGCAATTTCTGAA
GAAGACCAAAAAGAACCAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGCACACA
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCT
GACCTGTGACACCATTTTCATCCAGCACACGGAATCATCAAGATTGGCTCTGTGGCTCC
TGACACTATCAACAATCATGTGAAGACTTGTGAGAAGAGCAGAAGAATCTACACTTCTT
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTGAGGCAATGGAGAGTCCTCATATGT
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

FIGURE 2AAA

CATTCAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACCTCCTTGCGGCCCACTGCATTGTGGG
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAG
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC
TCAGTCACCAGCTCTGGAATTAGATAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA
GGTGGTGTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC
ACTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA
CAGTACCCTCAACTCAGCCGCTGTCAACGCTCTCCTCTTAGAGCTCACTCGGGCCAGGCCC
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC
AGTATTACCCTGTGAAGCCCCCTTCCCTCCTTTATTATTTCAGGAGGGCTGGGGGGGCTCCC
TGGTTCTGAGCATCATCCTTTCCCTCCCTCTCTTCTCCCTCTGCACTTTGTTTACT
TGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCGCCTTCTAGTTGGGGGCTAGT
CGCTGATCTGCCGCTCCCGCCAGCCTGTGTGGAAGGAGGCCCACGGGCCTAGGGGA
GCCGAATTCTACAATCCCGCTGGGGCGGCGGGGCGGAGAGAAAGGTGGTGTGCTGCAGTG
GTGGCCCTGGGGGGCCATTGATTGCGCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT
GCT

SEQ ID NO: 65_AA711829_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG
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ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAAACGGACTCATCAAG
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTAGGGCAAT
GGCGAGTCCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC
TCATTACAGAGGGAGTTTATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGGAGACCAACA
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC
AAGAACATGGATACCAGTGCTGTACTAGCTGAAATTCCCGCAGGGCCAGGACGAGAACCA
GTTCACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC
AGGAATGGGATCTACCCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCTGAGCCAGCT
GAAGTGGAGACACGAAAGGTGGTGTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC
TTCATTAGTGAGGCTGATCAGAGCCGCCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG
TTCAACTTCACCAGGAACAGTACACTCAACAGCCACTGTCAACGCTCTCCTCGTAGAGC
TCACTTGAGCCAGGCCCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCTCCT
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTTAGGAGGGCTTTAGGG
GCTCCCTGGTTGAGTATCACCTGCCCCCTTCCCTCTCTTCCCTCTGCACTTTGTT
TACTTGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGC
TAGTAGCTGACCTGCTGCCTCCTGCCCTACTTGTGTGGACAGGAGGCCACGGGCCTGG
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGTGCA
GGGGTGGCCCCCGGGGGGGGCATTGAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC
TTTTTGCT

FIGURE 2BBB

SEQ ID NO: 66_AA099102_H

ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCTC
TCATCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTCACCGAGTGTGAGCCG
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCTGGAGGCCGATGGCCAAGAG
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCACCTCTCCGGTCGCAAGCTGTCT
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC
TGCATCTGCCCGTCCCTGCCCTACTCACCCGTACGCTCCCCGCAGTCCTCGCCTCGGCTG
CCCCGGCGGCCGACAGTGGAGTCTCACCACGTCTCCATCACGGGTATGCAGGACTGTGTG
CAGCTGAATCAGTATACCCTGAAGGATGAAATTGGAAAGGGCTCCTATGGTGTGCTCAAG
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG
CTGATCCGGCAGGCCGCTTTTCCACGTGCGCCTCCACCCCGAGGCACCCGGCCAGCTCCT
GGAGGCTGCATCCAGCCCAGGGGCCCCATTGAGCAGGTGTACCAGGAAATTGCCATCCTC
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCTTGGATGACCCCAATGAG
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCACC
CTCAAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAGGGCAGT
GACGCGCTCCTCTCCAATACTACGTGGGCACGCCCCGCTTCATGGCTCCCGAGTCGCTCTCT
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA
TACTGCTTTGTCTTTGGCCAGTGCCCAATTCATGGACGAGCGGATCATGTGTTTACACAGT
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGCCGGAAATC
AAGCTGCACCCCTGGGTACAGAGGCATGGGGCGGAGCCGTTGCCGTGCGAGGATGAGAAC
TGCACGCTGGTCTGAAGTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC
GAGGGCAGCCGCGGGGAGGAACGCTCACTGTACAGCGCCTGGAACTTGCTCACCAAAAAA
CCAACCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT
CCAGGGCACCGACCCGCCCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC
TGCGTGGAAGTTGCTGGGCCCCCGCCCCGGCTCCCCCGCACGCATGCATCCACTGCGG
CCGGAGGAGGCCATGGAGCCCCGAGTAG

SEQ ID NO: 67_5R69_17_2_H

CCGGGATGTGAGCCTGGTGGTGGCAGCTGGAGCCACGTGCGAGGGGGGAAGTGTGCGCAGC
ATTCTCTGCAGGCATCACAGACCTGAGGCAGTGGCCTCCGGAGGGCACTGGACAGAAACA
GCCATCCAAGTGGCTGAGTGGAGGGACCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT
CCCTCAGGTAGGGATCGGGGCGCCTTGTGCGCCGACGCCACGTGTGGCGTCCGGTACAGT
CAGCAGAGTGCAGGGTGCGGGCACCGAGAAAGGGGCGCAGGGGAACCTCCCGCGGGCCTC
GCGTTTGGAACTTCTCGCCTGGGCAGGAGGCGGTGCTGGGAAAGAAGGTGGAAGAGCGA
TGGAATAATTTGAAGCATATTATCACCCCTTGCCAGGTTCATCCACAAACGGTGTGAAGAGA
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTTCAGCA
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG
TGAACAGGAAGCTGAGTGTGCTGGAAGGAGCTCTCGCTGTTACTTCAGGTTGAGCAAC
GCATGCCTGTTTACCCATAAGCCAAGGAGCGTCTGGGCACAGGAAGATCAGCAGGATG
CAGACGAAGACAGGCGAGCTTTCCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAACTTTGAGGCAGTGTAAGT
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAACTAGAAGTCATCAGTTTACTGGGAC

FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC
CACAGGTTTGGGGATCCATTCATGGCTAGCCAGGCTTCTGTCCATGGAATAACATGTGG
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT
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GGCCATGCAAAGAGGTAACATAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC
CAAGCTCTGGGTAAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG
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GGGCTGAGTCCATCAGAAGCCCCAGCCACCACAGCTCTGGTTCATGTAGTAGAGCTTCC
CACTCACACATCAAAATATGCCACCTCCCTTAGGACCCCTTCCTCTGCTCATTGACTCT
TTTGTCTTCTTCTCTCGGGGGTGAGGTGAGTTTACCACCAAATGCATGCAGGAGAT
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC
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CGGGACCCTGAGGGAGCTGTTGGATAGGGAAAAGACCTCACACTTGGCAAGCGCATGGT
CCTAGTCTTGGGGCAGCCCCGAGGCCTATACCGGTACACCATTGAGAAGCACCTGAACT
CCACGGAAAAATCAGAAGCTCAAACCTTCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC
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AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC
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CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAACTGGACATCTCTCTCTCAT
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CCTCTGACAGTAACTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT
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CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA
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GAGCTAAATAAATTACTGTTGTCTTTT

SEQ ID NO: 68_H85811_H

CGCCCCGGCCCCCTCCCCGGCGCCGGCCACGGGAGGCGGTGATGCGGGCGCGGGCGGCCT
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CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTTCTCCCTCACACCC
TTCAATCAAGTGCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAAGTGGG
ACATGACTGGGTACGGCTCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCCAAGCCTACCTT
ACGAGCAGACCATCGTCTTCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

FIGURE 2DDD

GCACTTCTGTCAACGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTCTGAAGCACTG
TGAGCCTCCTTGATACCTACCAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTGAGAATAATGCAAGCG
GGGCCACTGTGCGCCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG
AGGTCTTAGAGTTCTTGGGCCGAGGGACGTTTGGGCAAGTGGTCAAGTGTGAAACGGG
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GTCAGATTGAAGTGAGCATCCTGGCCCGTTGAGCACGGAGAGTGCCGATGACTATAACT
TCGTCCGGGCCTACGAATGCTTCCAGCACAAGAACCACACGTGCTTGGTCTTCGAGATGT
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TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG
AAACCCTGAACCATCCCTTTGTCCACCATGACACACTTACTCGATTTTCCCCACAGCACAC
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA
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GGCCAAGTGGGAGCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC
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TGGCCACGTGATGCGGCAGCAGCCAACCAGCACCACTCCTCCCCGGAAGAGTAAGCAGC
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCCTCTCAGGCCATCAGCT
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTGTGCCATGGTGCACA
GTAGCCCGCCTGCAGCACCTCGGTACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCA
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CTGTCTCCAAGCAAAGAAAAACGTATCAGCTGTGTACAGTCCACGACTCCCCCTACT
CCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGTGGGCACAACAATG
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GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCACCATGG
CCCAGGCTCCGTACTCCTTCCCGCACAAACAGCCCCAGCCACGGCACTGTGCACCCGCATC
TGGCTGCAGCCGCTGCCGCTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCACCTGGTGGCCTCGCAAGGCTCTG

FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA
GCATGGGCCCCCGGGTCCTGCCCTCGCCACCATCCACCCGAGTCAGTATCCAGCCCAAT
TTGCCCACCAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCAC
TGAGCCCCGCCAAGGTCAACCAGTACCCTTACATATAAACACTGGAGGGGAGGGAGGGAG
GGAGGGAGGGAGAGAATGGCCCGAGGGAGGAGGGAGAGAAGGAGGGAGGGCGCTCCTGGGA
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG
GGCGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTGGGACACCAGTGAAACTTGAACC
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTTTAAAAGGAAGGGATTAAAGAG
GGTGGGAAATCTATGGTTTTTATTTTAAAAAAG

SEQ ID NO: 69_DYRK3_H

CGGGAGCGAAAGTGCCTGAGCTGCAGTGTCTGGTCGAGAGTACCCGTGGGAGCGTCGCG
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GATCATACTCAGCACTTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA
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TCTCCTACTGTTTTCTCAGGGTAAAAGTTTCAGATTGCTTGAATACAGTAAAATCCAACAGT
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CACCACCTCACTGCCTATGAGAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTA
GGTCCAAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT
GATGCAGATGGGGCCTATATTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG
CTGAAAATTATTGGCAAGGGGAGTTTTGGGCAGGTGGCCAGGGTCTATGATCACAACTT
CGACAGTACGTGGCCCTAAAAATGGTGCGAATGAGAAGCGCTTTCATCGTCAAGCAGCT
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ATTCACTGCGATCTGAAGCCAGAAAACATTCTCCTGAAACACCACGGGCGCAGTTCAACC
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GAAACCAATGGTAGTATAACCCCTATGCAGTGTATTGCCAAAACCTGATTAGCTAGTGGACA
GAGATATGCCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAAATGGA
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AACATTTTTATATGATTATAAAGAATTCTTCAAGGGCTAATTACCTAACCAGCTTGTAT
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FIGURE 2FF

SEQ ID NO: 70_AA589241_M DYRK3_M

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GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTCATAGAGTTTC
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ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC
GGGTAGTTAAACCTACAAATGCTTTCAGGGACTGGGTTCGAAGCTGCCTCCAGTCGTTG
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GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT
GTATTTTTAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTAC
TGATGGATATGTTTTTGTAGACTTTTTTTTAAACAAGGCAGAACATTTTTATATGACTAT
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71_5R72_16_2_H

GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGCTGGGGCCCCCGGGCGCGGCCGGGACGA
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CGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCGGACCGGTCAAAGAGCCCCCTGA
AATCAATTTAGTTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA
TTTGAGGGTTAAATGCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAA
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAATCTCGCCTAGAAGAACTGGC
CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC
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TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAG
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CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTGAGGCCCTGA
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CTTCTTTAGTGAGACACAGAGACAGTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTG
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAA
GGGCGAAGTGACACTGCTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC
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FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA
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GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCAGTCCTTCCTGCCTGCTTCAGA
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TGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC
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TGGATTAGCTTATATCCATGAGAAAGGAATGATTACCGGGATTTGAAGCCTGTCAACAT
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AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC
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CAGAGATCCCCTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA
GAAATCAGTCATCTCTGGCTGTTGAACCACGATCCAGCAAAACGGCCACAGCCACAGA
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GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCACCATGATGGCCACAGAT
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GCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCTTTGTCTTCTAATAGTCT
GTGTGCACTCTACAAGTTTATTGAACAGAAGGGAGATTGCAAGATCTTATGCCAACAAAT
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GCTGATTCCCCAGTTTtagagggccacaagctctggggccagttcccaactgccattgggggt
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCTCAACATGGAGGAATCTGTTACAAT
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTGGTCAGATGTCTATGTCCAGGGCCATCAA
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CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATCTGAAGGG
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GAGTGTGCTAGCCCCGAGAAGCTGTGAGCCAGCACTAGGAGGCGCTATGAAACTCAGGT
ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAAT
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TGATGAACAGGCATTTAACACAACGTGTAAGCAGCTGCTGTACGCTGCCAAAGCAAAG
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGT
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAAACCCTAAAGAAC
TGTCGTTAACTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT

FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA
TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG
CCT

SEQ ID NO: 73_R43524_H, HRI_H

ATGCTGGGGGGCAACTCCGGGTCCGCAAGCGCAAGAGGAGGGCGACGGGGCTGGGGCT
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TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCCTACAACAGCCAACCTTCCCT
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AACAGAGCTATTACACACTTAATGAGGTCTGCTAAAGAGAGAGTTTCGTGAGGATCCTTGT
GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAACT
TCACGTTACTTAAATGAATTTGAAGAACTTGTCTCTTAGGAAAAGGTGGATACGGAAGA
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GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAA
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CAGCACTTAACGAGAAGGAACTCATCGCAGAGACCATCTGCCATTAGCTGCTGCAGAGT
GAACTTTTCCAAAATTCTGGAAATGTTAACCTCACCTACAGATGAAGATAATAGAGCAA
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SEQ ID NO: 74_17000057519457_H

CACAAGAGCCCTTCTGCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT
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AGACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTA
CGCCGGCCGATGGCGAGGAGCCCGCCCCGAGGCTGAGGCTCTGGCCGAGCCCGGGAGC
GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGT
TCCGTGGCCGCTTCCAGGGCCGCGCGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACC
GGCACCCGGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCCGGGCGC
TCCTCCGCTGTGCGCGCGCTGGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTT
CCAAGTCTTATATATGGAAGAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGT
CCACTATGGAGACTGAAAAAACTCCCCAGGGTCTCTCCAAGTTAGCCAAGACAATTGGGC

FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTCATGGTGATCTCACCACCTCCAACA
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT
TCATTTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCTGGAGAAGGCCCTTCC
TCAGTACCCATCCCAACACTGAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCT
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG
ATATTTTAAAGTGGTATGTGATCGTGTCAATTATCATCTGCACCTTCACTCAAGAGCTTACT
ATGTGTCTAAGTCATGTTCTAGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTT
CTCCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA
GAACATTATTCTCTTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC
GCTGAGCTTACTGGCCCTCTAACCAGTGTTTTTTTTTGTGTTGTTGTGTGATACATGTTAT
ATTTATTTTGAACCAGTTTAAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA
CAGCATGGAAAATATCAGTGTATTGTTTTATGAACTTTTCAGTGTATATATAGACCAAG
GATATGTGCTGAGTTTTGATGTCAAATATATTTCTCTTTCAGGGTCATGATCAAAAAATG
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC
TGAAATTCATGTTAACATGTTTTATTTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA
AGACAAGTGATTGATCTAAAGTTCCTTTTAAAGTTTATACCGCTAAACAACTGAGTTGAT
TTCTATCACAGGCAGTAAGTAGGTAGAGCAAAAATGGTGAAGTGAAGTGTGAAGACTGAA
GTTTGATGAAGTCTGGTTTAAAGGCACAGGTAACTGAGTGTGGATGCAAAAGTACCAGGA
GCTAGCTTTTAACTTGCCAGCCTCAGTTTCTTTTCTTAGAAGAAGCTATGTTTGGGTG
GGAAGGGAAGAGAGGGATAAGAAAATACCTTTCTTCTTGTAACTCCAATCAACAAACA
TATTTTGAGTGCCTTTTGTGTTCTTGGCACCTGTGGGTATTGGGTACTTGGCACCTT
GTTGGGTATTGGGTACAATGGTGAGCCAGACAGACACAGCGCCTGTCCTTTTGTAGAAT
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TGATTGCTACAGCTGAGCTAATTAACACCCATCACCTCACATAGTTACTGTCTTGTCTT
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TCAGTGCCTGTTCTTATGAAGCAAACATTCTATAATAGTAGGACCAGTACCCTGTCTGTT
TCATTACCACAGTCAGCATGCCCCAAGTGCCAGCATGGGGCGGATGGCCAGGAATGAG
TGAAAACCTCCCTTCCCTGGGTAGTTGTGACTAGTAGAGAGGAAAAATAATATAATTGCCT
GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTATATTGGATCTAAAATAACTCTTA
AGTTAGGCATTATCCCCATTTTATAGATGGAGAACTGGCCCCAAAAGGTGGGAACCTGT
CCAAGACGTCACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA
CTGACAAATGAGATATGGGATATGGTGCATCTTACAGTACTATAATAAGTATTGGCGTA
TAACATTATTTTCAAGGAACTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT
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SEQ ID NO: 75_AA013524_M

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GCCCCAGTCGTCTTCTTTGTGGAATATGCGTCTAACTGCTTATATATGGAAGAAATCGAA
GACTCGGTGACTGTTCTGGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG
TGCCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC
CTCATTACGGGGACCTCACACCTCCAACATGCTCCTGAGGCGGCCCCCTGGCGCAGCTG
CACATCGTGCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG
TTTGAAGCCTTTCTGAAGAGTTACGGGGCCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTTCGGGTAGTGGAGCTGT
GGTGAACCTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG
GGTTGTTAAGTGGTCTGTGATCGTGTGGGCCACCACCATCCATGGCTCACTGTTCTCAG
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT
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SEQ ID NO: 76_17000139801197_H, IRAKM_H

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CAGTGTAAGAAGCATTGGAAGAGGTTTTTATCTGAGCTTGAAGTTTACTACTGTTTCAT
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT
TATCCATACATGAGAAATGGAACACTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCC
CCACTCCCTTGGCACATTGGAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC
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SEQ ID NO: 77_AA840598_M IRAKM_M

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CACGTTTGAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGCACAACACT
CAGCCGTGCGCCGTCTCTGTGGCAACGTTTCCAGTGCAAACATACTCTTGGATGACCAG
CTCCAACCCAACTAACGGATTTTGTGTCAGCGCACTTCCGACCCAATCTAGAGCAGCAG
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACTGATGTCTACAGCTTCGGAATCGTGATC
ATGGAGGTTCTAACGGGCTGCAAAGTGGTGCTGGATGACCCGAAACACGTTTCAGCTGCGG
GACCTCCTCATGGAAGTATGGAGAAAAGAGGCCCTAGACTCCTGCCTGTCCTTCTTAGAC
AGGAAGATACCACCCTGTCCTCGGAACCTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG
TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCTGTCTCTCTGGAG
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TGTCTTCTCCACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAAC
CAGAATAACCATTAGTACCTCCCAAGGAAGTTTGGGGACAGATAGAGTGAAGTCAAGAA
ACCCCTTTGAATGCAGCCAGTCTGAGGTACCTTTCTAGGCTTGGACCGAAACAGAGGG
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CCAGAGCTTGTGGCGCCATCCCAGGACTTAAGTCCTACTGTGATCAGTTTGGGCTCGTCT
TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG
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AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCACTGATGGAGAATTTGAATGGTGCAG
ATTAGCAGCAAGGAAGTCTATTCTTCTCCAAACAGAATAATTTCAAGAGATGCTTTAT
TCAAGTGACCGCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC
AAGATTCCGGGTTCTGACAACCAAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT
AAGTCTCTCACTCTCTCTCATCATCCGAGTGAGATCTTGGTATAGGTGAACAGAGAACCA
CCCACCTTCCAGAACCAGAACCACCTTCTCCCAAGCCAGCAGTCAGTCACTCACCATCA
GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC
CTACGTCCTTTATAAAAACCAGGTCTTCAGGGCCCCACCCCTTTCTTTTTTCCATCCTTGCT
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TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTGAGATCATTGTCACAAGAACA
AGCGAATACACAACAACAAGGCCACCATCATTACCACCGGCCTTAATGCTAGTCTTTC
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TTTTACAGCCAGTTGCTACTCTTGTATTATCGCTGGTTAACCGGTCTGTCCGGAAGTGAGC
CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCCAGTCCAAAGTCTGCT
TCTCTGTATTTAAATTCTTAGAAGAGTTGCCTGTGGCATTCCAATTGTTATATAAAAAA
TTATATTAAAGAATTCCAGCACT

SEQ ID NO: 78_AA088547_H

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CTGCTGGTGTCCACCTTGGATGGAAGTCTCCACGCACTAAGCAAGCAGACAGGGGACCTG
AAGTGGACTCTGAGGGATGATCCCGTCATCGAAGGACCAATGTACGTACAGAAATGGCC
TTTCTCTCTGACCCAGCAGATGGCAGCCTGTACATCTTGGGGACCCAAAAACAACAGGGA
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GATGGGGTCTTCTACACAGGCCGGAAGCAGGATGCCTGGTTTGTGGTGGACCCTGAGTCA
GGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCGCTCTACATTGGC
CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC
ACCTACCGCGCTACTCAGCGCCCCCATGGATGGCTCACCTGGGAAATACATGAGCCAC
CTGGCGTCTGCGGGATGGGCCTGCTGCTCACTGTGGACCCAGGAAGCGGGACGGTGCTG
TGGACACAGGACCTGGGCGTGCCTGTGATGGGCGTCTACACCTGGCACCCAGGACGGCCTG
CGCCAGCTGCCGCATCTCAGCTGGCTCGAGACACTCTGCATTTCTCGCCCTCCGCTGG
GGCCACATCCGACTGCCTGCCTCAGGCCCCGGGACACAGCCACCCTCTTCTCTACCTTG
GACACCAGCTGCTAATGACGCTGTATGTGGGGAAGGATGAACTGGCTTCTATGTCTCT
AAAGCACTGGTCCACACAGGAGTGGCCCTGGTGCCTCGTGGACTGACCCTGGCCCCCGCA
GATGGCCCCACACAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT
GGACACCACGAGCTACCCCCAGTCCTGCACACCACCATGCTGAGGGTCCATCCCACCCTG
GGGAGTGGAAGTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG
GAGCTATTGAGCCTGAGCCGAGAGAACTTTGGGACTCCGAGCTGCATCCAGAAGAAAAA
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG
ACCCCCCTGGCACCTGCAGACTTTGCTCACATCTCCAGGATGCCAGTCCCTGCACTCG
GGGGCCAGCCGGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCCAGCCACTC
GACGACCTGAAGCTGAGCAACTCACCGTAGTGGGGAAGATTTCTTCAATCCCAAGGAC
GTGCTGGGCCGCGGGGACGGCGGGACTTTCTGTTTTCCGGGGACAGTTTGAGGGACGGGCA
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCCTGGTTTCGGCGGGAAGTTCAACTG
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCGAGCGGGGACCC
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCCCTCCTTGACAGGAGTACGTAGAAAAC
CCGGACCTGGATCGCGGGGGTCTGGAGCCCGAGGTCTGTGCTGCAGCAGCTGATGTCTGGC
CTGGCCACCTGCACTCTTTACACATAGTGACCCGGGACCTGAAGCCAGGAAATATTCTC
ATCACCGGGCCTGACAGCCAGGGCCTGGGCAGAGTGGTGCTCTCAGACTTCGGCCTCTGC
AAGAAGCTGCCTGCTGGCCGCTGTAGCTTCAGCCTCCACTCCGGCATCCCCGGCACGGAA
GGCTGGATGGCGCCCCGAGCTTCTGCAGCTCCTGCCACCAGACAGTCCCTACCAGCGCTGTG
GACATCTTCTCTGCAGGCTGCGTGTCTACTACGTGCTTTCTGGTGGCAGCCACCCCTTT
GGAGACAGTCTTTATCGCCAGGCAAACATCCTCACAGGGGCTCCCTGTCTGGCTCACCTG
GAGGAAGAGGTCCACGACAAGGTGGTTGCCCGGGACCTGGTTGGAGCCATGTTGAGCCCA
CTGCCCGACCCACGCCCCCTCTGCCCCCAGGTGCTGGCCACCCCTTCTTTTGGAGCAGA
GCCAAGCAACTCCAGTTCTTCCAGGACGTGAGTACTGGCTGGAGAAGGAGTCCGAGCAG
GAGCCCCCTGGTGGAGGCACTGGAGGCGGGAGGCTGCGCAGTGGTCCGGGACAACTGGCAC
GAGCACATCTCCATGCCGCTGCAGACAGATCTGAGAAAGTTCCGGTCTATAAGGGGACA
TCAGTGCGAGACCTGCTCCGTGCTGTGAGGAACAAGAAGCACCCTACAGGGAGCTCCCA
GTTGAGGTGCGACAGGCACTCGGCCAAGTCCCTGATGGCTTTCGTCCAGTACTTCACAAAC
CGCTTCCACGGCTGCTCCTCCACACGCACCGAGCCATGAGGAGCTGCGCCTCTGAGAGC
CTCTTCTGCCCCTACTACCCGCCAGACTCAGAGGCCAGGAGGCCATGCCCTGGGGCCACA
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SEQ ID NO: 79_HGP_6644466

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GGAAGGGATCAGTAATTTCAAGACACCAAGCAAAATATCAGAAAAAAGAAATCTGTATT
ATGTTCAACTCCAATAATAATATCCCGGCCTCTCCGTTTATGCAGAAGCTTGGCTTTGG
TACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTG
GGCTGTAAAAAAGATTAATCCTATATGTAATGATCATTATCGAAGTGTGTATCAAAAGAG
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TGCTTTTACTGAAGCCAATGATGGCAGTCTGTGCTTGTCTATGGAATATGGAGGTGAAAA
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CATAATTTTAAAAGTTGCTTTGAATATGGCAAGAGGGTTAAAGTATCTGCACCAAGAAAA
GAAACTGCTTCATGGAGACATAAAGTCTTCAAATGTTGTAATTAAGGCGATTTTGAAC
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TGGTGTATTACTGACAAGGCAGACATATTTGCCCTTGGCCTTACTTTGTGGGAAATGAT
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TGATGAAAGTGATTTTGGATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT
TAATATGGAAGAACTGGATGAATCATACCAGAAAGTAATTGAACTCTTCTCTGTATGCAC

FIGURE 2MMM

TAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA
TGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCCTAAATAACTGTTTATTCCAAAATA
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG
TTTCTTGTTAACATATGGATAACTATTTCTAATATGAAATATGCTTATATTGGCTATAAG
CACTTGGAATTGTACTGGGTTTTCTGTAAAGTTTTAGAACTAGCTACATAAGTACTTTG
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TGAATGACCATTACTTTTATTAATGATCTTTCTTAAATATTCTATATTTTAATGGATCTA
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAACACTGAACC
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA
GTAGCTCCTTGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGATCTCCTC
AGATCTTTGGTTTTTGTCTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAATTTA
TTAATTTGTACCTTAAGCATTTCCAGCTGTGTAAAAACAATAAACTCAAATAGGATGA
TAAAGAATAAAGGACACTTTGGGTACCAGAAGGTGTCTCAGCATTATTTTATACTTC

SEQ ID NO: 80_AA449542_M

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GTGCCTTGCTATGGAGTATGGAGGTGAAAAGTCTCTGAATGACTTAATAGAAGAGCGGAA
CAAAGACAGTGGAAGTCCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC
AAATGTTGTAATTAAGGTGATTTTGAACAATTAATCTGTGATGTAGGAGTCTCTCT
GCCATTGGATGAAAATATGACTGTGACTGATCCTGAGGCCTGTTATATTGGTACTGAGCC
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TGCTTTTGGCCTTACTCTGTGGGAAATGATGACTTTATGTATTCCACACGTCAATCTTCC
AGATGATGATGTTGATGAAGATGCAACCTTTGATGAGAGTGACTTCGATGATGAAGCATA
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TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA
TTAACTTGATGGAAGCTTTAACTAGATATATGTAGTTAATATAACTTATGGTAGCTAG
ATTCTAGAAGTAGCTTTAACTAGTAGTACCCTGTCTAAGATGACTTAAGAATCAAGGGA
CCATTGCTTTGTTACAGATCTTTTTAGATATTCTTGCTTCTTTAGTGGGTTACTAAAAAT
TTCACTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTGAGTCTCCTCAGCTGGC
CTGTCAGCCCATGCGCCCTGGGACTTGAGAAGAGTTTATAAACGTAGCTCCTAGGGTGTG
TTGCCTCTCTACACTTAGCTTCTAATTTATTACTTTGTTTCTACTGATTGTGTCTTAAGT
CTTTTAAATAAATGTAAGAATAAACAATAAAAGACAGTTTTAGTACCAGG

SEQ ID NO: 81_5R57_10_2_M TESK2_M

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SEQ ID NO: 82_AA232253_H

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GAGATGGATATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTAT
TTACATATGGAGGCTCCTGTCAAGGTGATTACAGAGACCTCAAGTCAAGAAACGTTGTT

FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT
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CTCCCTGTGTGAGAACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTA
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CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA
AAGCTGACAGAGCAGTCCAACACCCCGCTGCTGCCTTCCTTTGAGATTGGTGCATGGACG
GAAGACGATGTGTATTGGTGGGTTCAGCAGCTCGTCAGAAAAGGTGACTCTTCAGCAGAG
ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG
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AAGTCAGCCATTGAGAAATTAACCCATGATTACATAAATTTGTTTCACTTCCCACCACTA
ATTAAGGACTCAGGAGGTGAACCTGAAGAAAATGAGGAAAAAATAGTGAACCTGGAACCTG
GTTTTTGGTTTTCACTTGAAACCAGGAACCTGGCCACAGGATTGTAAGTGGAATAATGTAT
ATGGAGATGGATGGGGATGAAATTGCAATAACCTACATAAAAGATGTGACATTCAACACT
AACCTACCTGATGCGGAGATTTTAAAGATGACAAAGCCACCATTGTATGGAGAAGTGG
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AGAACTCCAAAAAGCACTAAACATGTCCATTTGATTCACTGGAGTAGAACAACCTCAG
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TTCTTCTCACACTTTGATGGCCAGGATTCTACGCTGCTGCTGTGAGACGGCCCCAGGTG
CCCATTAAGTATCAACAGATTACACCTGTGAACAGTCCAGAAGCTCGTCTCCTACTCAG
TATGGACTGACCAAAAACCTTCTTCTTACATCTCAACTCTAGGGACAGTGGCTTTTCC
AGTGGCAATACTGACACCTCTTCAGAGAGGGGTGCTACTCAGACAGAAGCAGGAACAAA
TATGGACGTGGTAGTATATCACTCAATTCTTCTCCTAGAGGAAGATACAGTGGAAAGAGT
CAGCATTCCACTCCATCAAGAGGAAGATACCCTGGAAGTTCTACAGGGTTTCTCAGTCA
GCACTCAATCCTCACCAGTCGCCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC
AACACCATAACCAGGGATGCCTTTGCACCCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGGAATACCGGAAAAAGCCCCACAGGCCA
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TGA

SEQ ID NO: 83_AI375137_H

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GAACTGACAGAATAAGGAATATATTTGGCTCTGATGAAGCCTTCAGTAAAGTCAATTTA
AATTACCGCACTGAAATGGGCTGTCTCTACTTCATTTATGTTGCATTTGTGGAGGCAAG
AAATCACATATTCGAACTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAAT
GGATTTACAGCCTTGCAATTTAGCAGTTTACAAGGATAATGCAGAAATGATCACTTCTCTG
CTTCACAGTGGAGCTGATATACAGCAGGTTGGATACGGTGGCCTCACTGCCCTCCATATT
GCTACAAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC
AATATTCAAGATGCAGTTTTTTCACTCCATTGCATATTGCAGCGTACTATGGACATGAA
CAGGTAACCTCGCCTTCTTTTGAAATTTGGTGTGATGTAAATGTAAGTGGTGAAGTTGGA
GATAGACCCCTCCACCTAGCATCTGCAAAAGGATTCTTGAATATTGCAAACTCTTGATG
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCACTCCAT
TTCTGTCTCGATTTGGACACCATGATATAGTTAAGTATCTGCTGCAAAGTGATTTGGAA
GTTCAACCTCATGTTGTTAATATCTATGGAGATACCCCTTACACCTGGCATGCTACAAT

FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG
GAAAACATCTTCAGTGAAACAGCTTTTCATAGTGCTTGACCTATGGCAAGAGCATTGAC
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG
CACACTGGATTACACTCTGCTTGCTACCACGGTCACATTGCGCTGGTTTCAGTTCTTACTG
GATAATGGAGCTGATATGAATCTAGTGGCTTGATGCCAGCAGGTCTAGTGGTGAAAAA
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTACACTC
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA
GGAGATGGCTCCTATGTGTCTGTTCCATCACCTTGGGGAAGATTAAAAGCATGACAAAA
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCTTCACATTTCCATCTTCAGCTC
TCAGAAATTGAGTTCCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG
TCAGATGTGGATATGTTTTGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCATCCCTGC
GTAATTCAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA
TACATATCAGGGGGTTCTCTGTTCTCCCTCCTTCATGAGCAGAAGAGGATTCTTGATTTG
CAGTCTAAATTAATTATTGCAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG
ACACAGCCAATTATACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGG
CATGCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC
ATGACAAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACGCAGTGCCT
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT
GGCGAAATTCCATTGCTCATCTCAAGCCAGCGGCTGCGGCAGCAGACATGGCTTACCAC
CACATCAGACCTCCCATTTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA
GGGTGGAACGCATGTCTGAAGGAAGACCCGAATTTTCTGAAGTTGTATGAAGTTAGAA
GAGTGTCTCTGCAACATTGAGCTGATGTCTCCTGCATCAAGTAACAGCAGTGGGTCTCTC
TCACCTTCTTCTTCTTCTGATTGCCTGGTGAACCGGGAGGACCTGGCCGGAGTCATGTG
GCAGCATTAAGAAGTCGTTTGAATTGGAATATGCTCTAAATGCAAGGTCCTATGCTGCT
TTGTCCCAAAGTGCTGGACAATATTCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG
CATTTTCATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCAGCTGA

SEQ ID NO: 84_H97685_H

ATGATTTCTTGCTGTNATAACCTATGCACTCACAAGATGAAGTCTCTGAGAGGGATGA
GCAAGAGCTTCAGGAAATCCGAAAGTATTTCTCCTTTCTGTATTCTTTTTCAAAGTGCC
GAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAATGGAGAGCGAAAGATCACC
GCTTTATCGCCAGCTAATTGACCTGGGCTATCTGAGCAGCAGTCACTGGAAGTGTGGGGC
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGGAACAGAGTGAAAAGCTGAGACA
CTTGAGCACATTTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT
GAACCTGGTGCCTGCACTGCCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAAGGAGAATGAGTTGTA
TGAATCATTGATGAATATTGCCAACCGAAAGCAGGAGGAAATGAAGGATATGATTGTTGA
GACACTTAATACCATGAAGGAGGAACCTCTGGATGATGCTACTAACATGGAGTTTAAAGA
CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG
ACAGATCCAGGAACTCATCATCTCCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG
CTCAGTGGATTACCTGAGGGAAAGCTTCGTGCGGAACCTGGAACGATGTCTGCAGAGCCT
GGAGAAGTCTCAGGATGTCTCAGTTCACATCACCAGTAATTATCTCAAACAGATCTTAA
TGCTGCCTATCATGTTGAAGTCACGTTTCACTCAGGGTCGTCACTTACAAGGATGCTATG
GGAGCAAATCAAACAGATCATCCAGCGCATCACATGGGTGAGCCCACCTGCCATCACTCT
GGAATGGAAGAGGAAGGTGGCCCAAGGCAATTGAGAGCCTCAGCGCCTCCAAATTGGC
TAAGAGCATTTCAGCCAATTCCGGACTCGGCTCAATAGTTCCACGAGGCTTTTGCAGC
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGGTTAGAGAAAACGGAAGATCTATG
GCTGAGGGTTGCGAAAGATCATGCTCCCCGCTGGCCCGCTTTCTCTGGAAGCCGTTCT

FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA
GTATGGTGTGGTATACCTGTGTGACAACTGGGGAGGACACTTCCCTTGTGCCCTCAAATC
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTTCACTATATGAG
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTCAGTCATTGACTACAACATA
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA
CACAGGGCTGAAGGCTGGGCTGACCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT
GGAGGGAATCCGCTTCCCTGCACAGCCAGGGACTTGTCCATCGTGATATCAAACCTGAAAAA
TGTGCTGCTGGATAAGCAGAACCGTGCCAAGATCACTGACTTAGGATTCTGCAAGCCAGA
GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCCTGAACTTTTCAC
AGGGAAGTACGATAATTCCGTGGATGTCTACGCTTTTGGAAATCTTTTCTGGTATATCTG
CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG
GAACAATGTGCGGAGGGGGGCTCGCCAGAACGCTTCTCCTGTGTTTGATGAGGAGTGCTG
GCAGTTGATGGAAGCCTGTTGGGATGGCGACCCCTTGAAGAGGCCTCTCTTGGGCATTGT
CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTCACTCTCTAGTTATT
TCCTTCCCCCTCACCATTGCGCATGGGGAGAATTTGACATTTATTCACTATAGGACACA
CTCCCAAGGGAAGTGGTGTCTGCTGGGAACTTGGAACTTCCAGGCAGGGATGACTCC
TGGACAGTGAAGAGTTGAATGACTGAGCATATTCAGCAGCTCACTGAAGCGCCAAGCTAT
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SEQ ID NO: 85_W20810_M

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CTCCCGGCTTGGAAAACTGAAGGAGTTAATGATTCATTGCTGGGGTTCCTCAGTCCGAAA
ACAGGCCATCCTTCCAGGACTGCGAACCAAAAACCAATGAAGTTTACAATCTGGTAAAGG
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GCAGAAACTTGTCTGCCAGAGAGCCAAGCCAAAGAGGCACAGAAATGGATTGCCCGAGGG
AAACCATGGTTTTCTAAAATGCTGGACCGCTGCATTTGGAGGAACCTCCGGACCAGTTC
CTGGAAAAATGCTCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAGCAA
GGACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCCTTCAGAG
GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCTCACCCTTCAAGGAATCAGG
GAGATGGAAGACACGGCACTCCTTGGTATCCCTGGACCCACCGAATCCAATGACAGGGC
CACCGGCTCTCGTCTTCAACAACCTGTTCTGAAAGTGCAGATTGGGAACTACAACCTCCTGG
TAGCACCACCAAGAACTACTGCCTCAAGTTCCGGCCAAGTATGACCAAGCACAGTTCCGGCA
GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGA
AGTGTGCCATTTCAGCGTGGCAATAAAAAGCACGTTTTTAAGCAACCTGGACTGGCTAAGAC
AGTCCTTGCCACTTCTGAAAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAA
ACTGACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTG

SEQ ID NO: 86_AA744236_H

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GTGTATAAGAGAGAAAATGAAGACAAGGTTAATAAAGCTGCCAAGCATTGGAAGACACTT
CGTCACCCCTTGCTTGCTAAGATTTTTATCTTGTACTGTGGAAGCGGATGGCATTTCATCTT
GTCACTGAGCGAGTACAGCCCCCTGGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCTTCATGACAGAGGACACCTA
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGACACTGGAAGCTA
GGAGGAATGAAACTGTTTGTAAAGTTTCTCAGGCCACACCAGAGTTTCTGAGGAGTATT

FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACCT
CTCCAGAGTGTGATGGACATGCCCCGGGATGCCTTTTCATTTGGAACATTGGTGGAAGT
TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC
TTGCACTCAACTTTGCTGAATCCCATTTCCAAAATGTGCGCCAGCGCTCTGCACCTTACTA
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAACA
TTGAAGAGTGAAGAGGAGAAAACGGAATTCCTTAAATTTCTGCTGGACAGAGTCAGCTGC
TTGTGAGAGGAATTGATAGCTTCAAGGTTGGTGCCTCTTCTGCTTAATCAGTTGGTGT
GCAGAGCCAGTGGCTGTTAAGAGTTTCTTCTTATCTGCTTGGCCCCAAAAAGATCAT
GCGCAGGGAGAACTCCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC
GTGCTTCTCCAGTTGTTTGAAGTTCATGAAGAGCATGTGCGGATGGTGCTGCTGTCTCAC
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GTTTTGCTGGGCCTGCGTGATACTAGCGATTCCATTGTGGCAATTACTCTGCATAGCCTA
GCAGTGCTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAACGAACCAAGATC
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GACAGTGAAAACCTCCCATCAAGTCTAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA
CCTGAGGAGCCTGAAAATCAAACGTCAACATACAGATTTGGCCTAGAGAACCTTGATGAT
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CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT
ACCTCAGGGGAGCAGAAGCCTATTCTGCTTTGCTTCACTCACTGAAGAGTCTATGCCT
TGGAATCAAGCTTACCCCCAAAAGATTAGCCTTGTAACAAGGGGGGATGACGCAGACCAA
ATCGAGCCGCCAAAAGTGTATCACAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT
TTAGGAGAGGAATTCACCATTCAAGTAAAAAAGAAGCCAGTAAAAGATCCTGAGATGGAT
TGTTTTGCTGATATGATCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA
CTGAGGACAGAAATGGTCCCAAAAAGGATGATGTCTCCCCAGTGATGCAGTTTTCTCA
AAATTTGCTGCAGCAGAAATTACTGAGGGAGAGGCTGAAGGCTGGGAAGAAGAAGGGGAG
CTGAAGTGGGAAGATAATAACTGGTGA

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CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGCAG
TAATGGGAATTCCTGTCACTAGAGAATTTGATGTTGGTCGACACATTGCCAGTGGTTGCA
ATGGGCTAGCTTGGAAGATTTTAAATGGCACAAAAAAGTCAACAAAGCAGGAAGTGGCAG
TTTTTGCTTTGATAAAAACTGATTGACAAGTATCAAAAATTTGAAAAGGATCAAATCA
TTGATTCTCTAAAACGAGGAGTCCAACAGTTAACTCGGCTTCGACACCCTCGACTTCTTA
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ACATTAAGGATTATAAACTTTATGATGTAGAAACCAAATATGGTTTGCTTCAGGTTTCTG
AAGGATTGTCAATCTTGATAGCAGTGTGAAAATGGTGCATGGAAATATCACTCCTGAAA
ATATAATTTTGAATAAAAGTGGAGCCTGGAAAATAATGGGTTTTGATTTTGTGTATCAT
CAACCAATCCTTCTGAACAAGAGCCTAAATTTCTTGTAAAGAATGGGACCCAAATTTAC
CTTCATTGTGTCTTCCAAATCCTGAATATTTGGCTCCTGAATACATACTTTCTGTGAGCT
GTGAAACAGCCAGTGATATGTATTCTTTAGGAACTGTTATGTATGCTGTATTTAATAAAG
GGAAACCTATATTTGAAGTCAACAAGCAAGATATTTACAAGAGTTTCAGTAGGCAGTTGG
ATCAGTTGAGTCGTTTAGGATCTAGTTCACTTACAAATATACCTGAGGAAGTTTCGTGAAC
ATGTAAAGCTACTGTAAATGTAACCTCGACTGTAAGACCAGATGCAGATCAAATGACAA
AGATTCCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC
AAAGAGATAATCTTCAGAAATCACAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAAC

FIGURE 2RRR

TGCCCAAGCGTGTCATTGTGCAGAGAATTTGCTTGTGTTGACTTCAGAATTTGTAAACC
CTGACATGGTACCTTTTGTGTTTGCCCAATGTTCTACTTATTGCTGAGGAATGCACCAAAG
AAGAATATGTCAAATTAATTCTTCCTGAACCTGGCCCTGTGTTTAAGCAGCAGGAGCCAA
TCCAGATTTTGTAAATTTTCTACAAAAAATGGATTGCTACTAACCAAAACCCCTCCTG
ATGAGATAAAGAACAGTGTCTACCCATGGTTTACAGAGCACTAGAAGCTCCTTCCATTC
AGATCCAGGAGCTCTGTCTAAACATCATTCCAACCTTTGCAAATCTTATAGACTACCCAT
CCATGAAAAACGCTTTGATACCAAGAATTAATAATGCTTGCTACAAACATCTTCCCTTGC
GGTTCGTGTAAATTCATTAAACAACATTGGAGCAGACCTTCTGACTGGCAGTGAGTCCG

SEQ ID NO: 88_AA278842_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCCCCGGCTCGGGCGGCCGGAG
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GGGACCCGGTCCGGGACTTTCCGTTTCGAGCTCATCCCGGAGCCCCAGAGGGCGGCCTGC
CCGGGCCCTGGGCCCTGCACCGCGGCCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA
AGCGCTTCAAACTCTACGGCACCCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG
AAAAATGCCTCCACGTGCTGACAGAGGCTGTGACCCCGTTGGGAATATACCTCAAGGCGA
GAGTGGAGGCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGTGA
AAGCCCTCAGCTTCTGGTCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCG
CCGTGTTCTGGACCGAGCTGGCGAGTGGAAGCTTGGGGGCTGGACTACATGTATTCGG
CCCAGGGCAACGGTGGGGGACCTCCCCGCAAGGGGATCCCCGAGCTTGAGCAGTATGACC
CCCCGGAGTTGGCTGACAGCAGTGGCAGAGTGGTCAGAGAGAAGTGGTCAGCAGACATGT
GGCGCTTGGGCTGCCTCATTTGGGAAGTCTTCAATGGGGCCCTACCTCGGGCAGCAGCCC
TACGCAACCCTGGGAAGATCCCCAAAACGCTGGTGGCCCATTAAGTGTGAGCTGGTGGGAG
CAAACCCCAAGGTGCGTCCCAACCCAGCCCGCTTCTGTCAGAACTGCCGGGCACCTGGTG
GCTTCATGAGCAACCGCTTTGTAGAAACCAACCTCTTCTGGAGGAGATTAGATCAAAG
AGCCAGCCGAGAAGCAAAAAATTCTTCAGGAGCTGAGCAAGAGCCTGGACGCATTCCCTG
AGGATTTCTGTCGGCACAAGGTGCTGCCCCAGCTGCTGACCGCCTTCGAGTTCGGCAATG
CTGGGGCCGTTGTCTCACGCCCCCTCTTCAAGGTGGGCAAGTTCCTGAGCGCTGAGGAGT
ATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGC
GCATCCGCCTCCTGCAGCAGATGGAGCAGTTCATCCAGTACCTTGACGAGCCAACAGTCA
ACACCCAGATCTTCCCCACGTGCTACATGGCTTCTTGGACACCAACCCTGCCATCCGGG
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TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA
GGGTCTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGCACCGTCCCGGGTTG
CGGGTGTCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGA
AGATCCTGCCTGTGCTCTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGG
CCTTCAAGGCCATTTCGGAGCTTCTGTCCAATTTGGAGTCTGTGTGCGAGGACCCGACCC
AGCTGGAGGAAGTGGAGAAGGATGTCCATGCAGCCTCCAGCCCTGGCATGGGAGGAGCCG
CAGCTAGCTGGGCAGGCTGGGCCGTGACCGGGGTCTCCTCACTCACCTCCAAGCTGATCC
GTTTCGCACCCAACCACTGCCCCAACAGAAACCAACATTCCCCAAAGACCCACGCCTGAAG
GAGTTCCTGCCCCAGCCCCACCCCTGTTCTGCCACCCCTACAACCTCAGGCCACTGGG
AGACGCAGGAGGAGGACAAGGACACAGCAGAGGACAGCAGCACTGCTGACAGATGGGACG
ACGAAGACTGGGGCAGCCTGGAGCAGGAGGCCGAGTCTGTGCTGGCCAGCAGGACGACT
GGAGCACCGGGGGCCAAGTGAGCCGTGCTAGTCAGGTGAGCAACTCCGACCACAAATCCT
CCAAATCCCAGAGTCCGACTGGAGCAGCTGGGAAGCTGAGGGCTCCTGGGAACAGGGTT
GGCAGGAGCCAAGCTCCCAGGAGCCACCTCCTGACGGTACACGGCTGGCCAGCGAGTATA
ACTGGGGTGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCTGTCTGCACGTC
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCCGAAGAAGCGCGAGGAGCGGCGGCGGGAGA
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCCGA
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGCTGCGGAGAGCCCCGCCACAGATGT
ATTTATTGTACAAACCATGTGAGCCCCGCGGCCAGCCAGGCCATCTCACGTGTACATA
ATCAGAGCCACAATAAATTCTATTTTAC

SEQ ID NO: 89_AA599286_H

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CAAGGAGGAATTTCTGTGGAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCCTCCCAAAAAATTG
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTAGAT
CCAAACAACCTATTCCGCAAACTATACTGAGATTGCCTTGCAACAGGTTTCCATGTTCTTC
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACTTTGAAAGACATAGGTTGGAGAATAAGG
AAGAAATATTTCTTGATGAAGATTAATAATCAGCCAAAGGAACGGCTAGTGTTAAGCTGG
GCTGACCTTGGCCGAGACAAGTATTTGTGAGATAAAGATTTTCAGTGTCTAATCAAACCTT
CTGCCTTCTTGTGTTGCACCCTTACATCTATCGGGTTACCTTTGCCACAGCTAATGAATCC
TCAGCGTTGCTAATTAGGATGTTTAAAGAAAAGGGAACATTGAAGGATCTGATCTACAAG
GCAAAACCAGAAAGACCCATTTCTAAAGAAGTACTGCAACCCTAAGAAGATTCAGGGCCTG
GAACTCCAGCAAATAAAAAACATATGGACGGCAAATATTAGAGGTACTGAAGTTTCTTCAT
GACAAGGGATTCCCTTATGGGCATCTTCACGCCTCCAATGTGATGCTCGATGGGGACACT
TGCCCGCTGCTGGACCTTGAGAATTCCTTATTGGGCCTGCCTTCCTTCTACCGATCTTAT
TTTTTACAATTTCAGGAAAAATCAATACATTGGAAAGTGTGGATGTCCACTGCTTTGGCCAC
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CCTGCCCCGTCCATGGCTGTGGTGGCCGTGTTGGAGTCTACGCTGTCTTGTGAAGCCTGT
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CTAACCACTTCTGAAAAACCACAGTTTAAAGATCCCTACAAAGTTAAAAGAGGCATTGAGA
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CGAAGACTGACAAGAGCTCAGTCCACCATGGATCTGAGGAGGAAAGAAAAAAGAAAG
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TCATCGCCAACCTCCACCCTCTACATCAGGGATATCTGCATTACCTCCACCTCCTCCACCT
CCACCACCAGCAGCTCCCTTGCCCTCTGCGAGCACCGAGGCACCTGCCCAGCTCTCG
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCCCTTGCTCAGCTCCATCCAGAATTTCAA
AAAGGAACCTTTGAGGAAAGCCAAACCTGTGATCACAGTGCTCCGAAGATCGGCTGAAGCT
TCCTGTTTACACTTGGAGGGAAAAGTTCTTTTTTATTCTACTACCCCTACCCCCAAC
TACCCTCTTCTGGGAAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC
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SEQ ID NO: 90_AA425725_H

ATGAGCGCCAGCACGGGCGGTGGTGAGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC
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TACTGCAAGGGCGGCTACCACCCTGTGAAGATCGGCGACGTGTTCAATGGGCGGTACCAC
GTGGTGCGCAAACTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCGGGGCATTACACGGAGACAGCT
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCAGTGACCCCAAAGA
GAGACCATTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

FIGURE 2TTT

TGCATGGTGTCTGGAGGTGCTGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACTAC
CAGGGCCTGCCCCGTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCGAGAACATCTTGCTG
TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGCCACGGAGTGGCAACAGGCA
GGGGCGCCGCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCAGGAGGTCTTGACCGGT
AAGCTGTCCAAAAACAAGAGGAAGAAGATGAGGCGCAAACGAAACAGCAGAAGCGGCTG
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT
GAGGACTCTGGCTTGAGACTAGACGGGGGCGAGCGGCTCCACATCCTCTTCAGGCTTCTCC
GGCTCCCTCTTCTCTCCTGCCTCCTGCTCCATCCTCTCCGGCTCGTCCAATCAGCGAGAG
ACCGGGGGCCTCCTGTCGCCTAGCACACCATTGCGGTGCCTCGAACCTCCTGGTGAACCCC
CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC
GAGCTGGCCACTGGTGACTACCTGTTTCGAGCCGATTCTGGAGAAGACTACAGTCGTGAT
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGACATCCCCCAGCCTTCGCCCTC
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT
CTCAAGCACTGGGGCCTGTACGAGGTACTCATGGAAAAGTACGAGTGGCCCCCTAGAGCAG
GCCACACAGTTTCAGCGCCTTTCTGCTGCCCATGATGGAGTACATCCCCGAAAAGCGGGCC
AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

SEQ ID NO: 91_SGK022_H

TCTGGCCCTGTCCCTCCCCACCACCCGCGCTGTGTCCAGACAGAGAATGTTCTAACGCT
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GTAGAGCTGCCTCTCAGAGGCAGCATGAGCTGAGAGGGTGATAGGAAGGCGGCGCTAGAC
AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG
ACCTACTCAAAAGTCAAAGAAGCATTTCACAAAAACACCAAAGAAAAGTGGCAATTTAA
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCTCCCTCGGGAGCTC
CAAATCGTCCGTACCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT
GCCGACGGGAAAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC
GTGCTGAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTCAGATGGTT
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAAC
GCCTTGTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCC
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAG
GTGCTGCAGGGCATTCCCCACGATAGCAAAAAGGTGATGTCTGGAGCATGGGTGTGGTC
CTGTATGTCTATGCTCTGTGCCAGCCTACCTTTTGACGACACAGACATCCCCAAGATGCTG
TGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT
AGTTGGCATCCATGGCTAGCAAGCACTTGATAAAAGCAATGGCAAGTGCTCTCCAATAAA
GTAGGGGGAGAAAGCAAA

SEQ ID NO: 92_AA060026_M SGK022_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGGGGGGAAAAGA
AGCAGGCCGAGGGCGATGGTGAGTAGAGCTGCCTCGCAGAGGCAGCATGAGCTGAGAGG
GTGACAAGAAGGAGGCGCTACACAGCATGGAGGACTTTCTACTCTCCAATGGGTATCAGC
TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAGTCAAAGAAGCATTTCACAAAAAC
ATCAAAGAAAAGTGGCAATTTAAATATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC
AGAGATTCTGCCTCGTGAGCTCCAGATTGTCCGTACCCCTGGACCACAAAAACATCATCC
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAATCTACCTGGTGATGGAACTGGCTG
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGCCA
AGGCCCTCTTCCGCCAGATGGTTGAGGCTATTGCTATTGCCATGGCTGTGGCGTGGCCC

FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA
GCACAGCCTATGCCGCCCCCTGAGGTGCTACAGGGCATACCCCATGATAGCAAGAAAAGTG
ATGTCTGGAGCATGGGTGTGGTCCTGTATGTAATGCTCTGTGCAAGTCTACCTTTTGATG
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC
TCCGGCCTTCAATCGAAGAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC
AATGGCAAGTCCTCCCCAATAAAGTAGGGGGAGAAAGCAAAC TG

SEQ ID NO: 93_AA399669_H

CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCCGGCCGCACTTCATTCTCAA
GTTTTGTGGCCAACGATGGATAGGAGGTGGATTGTGATGTATTGGAACATGGGACCTTG
AGGAGTTCCGTAACCAAAAGGAGAAAGTAACAACAGCCAGTGGAGACAAAAGAACTGCT
TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGGAGGGCTGAGTCCAGCATCCCAGACTCGT
GTGACTATATAGGCAAGCATTGTTGGGACCTACTTCACTTTGATACCCTAGCCTTCAGCAG
CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA
AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACCACAGCCTACC
ATTCCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCCGTGAAATACAGGTAA
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC
GAGTATACATCATTCTGGAACCTGGCTCAGGGTGGTGATGTCTTGAATGGATCCAGCGCT
ACGGGGCCTGCTCTGAGCCCCCTTGCTGGCAAGTGGTTCTCCAGCTGACCCTGGGCATTG
CCTACCTGCACAGCAAGAGCATCGTGCACCGGACTTAAAGTTGGAGAACCTGTTGCTGG
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTCTTTTCCCACCTCAGCCAGA
CTTACTGTGGCAGCTTTGCTTACGCTTGCCAGAGATCTTACGAGGCTTGCCCTACAACC
CTTTCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTACTCTAGTGGTCGCCCATC
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT
TCCCAGCTAACCATAACCATCTCCCAGGAGTGCAAGGTCCAAGTCTCATTGCCTGTGTGG
CACAATGGAGAAAACTCAGGCAAGACCTCTCTCTCCCCTGCTCTAGAACCTGATCCTCC
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCCTGGG
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94_AA758539_H

GACCATTGAGACGCTCCGGTAGTGTAATGAGGACAATGCCTGCTGGCCACATGACGG
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AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGCAAGGGTTCCTACGCAAAAGTCAA
ATCTGCCTACTCTGAGCGCCTCAAGTTCAATGTGGCTGTCAAGATCATCGACCGCAGGAA
AACACCTACTGACTTTGTGGAGAGATTCTTCTCGGGAGATGGACATCCTGGCAACTGT
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC
CCTGCATGAGGACGTGGCACGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGAGAACCTTCTCCTCGACAAGGA
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTCGGCAGCATATGCAGCCCCCGAGGTGCT
GCAGAGCATCCCCACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA
CCTCATCTACCGCATGCTGCAGCCCGACGTACGCCAGCGGCTCCACATCGATGAGATCCT
CAGCCACTCGTGGCTGCAGCCCCCAAGCCCAAAGCCACGTCTTCTGCCTCCTTCAAGAG
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAACCTGGACACCAAGACAGGCTTGAGGCC
CGACCACCGGCCCGACCACAAGCTTGGAGCCAAAACCCAGCACCGGCTGCTGGTGGTGCC
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG
TGGTGGGGGTGCGGGTTGGGGGGCATGGTGCACTCGGCCTTACGTAAACTAAGTAGGCA
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAATTCGTCAATTAAACCACTATTTTGA
TT

SEQ ID NO: 95_AA883975_H

ATGTCGGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCCGCACAATTGGAGAG
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AAGGTGGTGGACCGGCGGCGAGCGCCCCCGGACTTCGTCAACAAGTTCTTGCCGCGAGAG
CTGTCCATCCTGCGGGGCGTGCGACACCCGACATCGTGACGTCTTCGAGTTCATCGAG
GTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCGGCCACCGACCTGCTGCAAGCC
GTGCAGCGCAACGGGCGCATCCCCGGAGTTCAGGCGCGCGACCTCTTTGCGCAGATCGCC
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCAGAAAC
GTGCTGCTGAGCCCGGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG
GCCCCATGGCTACCCAGACCTGAGCACCACTACTGCGGCTCAGCCGCCTACGCGTCAACC
GAGTGCTCCTGGGCATCCCCTACGACCCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC
GTGCTCTACGTATGGTCACCGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
AAGGCCCTGATCGCCGAGCTGCTGCAGTTCAGCCCGTCCGCCAGGCCCTCCGCGGGCCAG
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGACTCCGGCTAG

SEQ ID NO: 96_AA905446_H

CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA
TCATGGAAAGAATTGTGGGGTCAGGGGACAGTGGCGGGAGGAGCTGGCTCACCACCCTGT
GGACAAATCAGGCCTTATAATTTGTGATTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC
TTTTGAATGATATACTAACGACAAAAATAATAGAAGTGAACATTCTTTGCAATGTCCAAG
CAGCTAGACACACTTAAGACCATTAAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC
AGAAGTTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCTTTCTGATCTGCCAGCCCAT
CTCTCCTCCCTTACTTCCTCAGAGTTTATCCAGAGATTCTCCTCCCTCGGGAGCTCCAAAT
CGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCTGCCGA
CGGGAAAATCTGCCTGGTGTGAGGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT
GAATGGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTCCGTGAGATGGTTGAGGC
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT
GTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCCAAGTC
ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT
GCAGGGCATTCCCNCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCA
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC

FIGURE 2WWW

SEQ ID NO: 97_H29974_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTTATGAGGCAGTGGC
CGGGCGCAGCGGGCCCCGGGTGGCGGTCAAGAAGATCCGCTGCGACGCCCCCGAGAACGT
GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT
CGTGCACTTTGAGGAGTGCCTCCTGCAGCGCAATGGGTAGCCCAGCGCATGAGTCACGG
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT
CCTGGGTATATGCTGAGGAGCCCTGCTATCTCTGGTTTTGTCATGGAGTTCTGTGAAGGTGG
AGACCTGAATCAGTATGTCCTGTCCCGAGGCCAGACCCAGCCACCAACAAAAGTTTTCAT
GCTACAGCTGACGAGCGCCATTGCCTTCCTGCACAAAAACCATATTGTGCACAGGGACCT
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGA
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTTCGGACTTCTA
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCT
AGAAAACCCAAAGATGGAGTTGCACATCCCCCAAAAACGCAGGACTTCCATGTCTGAGGG
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCCTGATGCCTT
TGAACCTGAAACCAGAATGGACCAGGTACATGTGCTGCTTAAATTCAGGGCTAAGCAT
TTTGGGTGATTTTAACTAGGTTCGATTCTCGGGACCCACAGTCTCACCACGTCTCCTCC
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGGTTGGCGATCTCCCGACAGCTGGA
TCCGGCAATGTGAAGCTTTTGTGTTGGGTTTCCCCGCTTCTTTTATGTTTTGCTTTATTN
TNCCCTTTTCTTTCTTTTNTTNNCCACNTNCCTTTTAAATTTAAACCATTTGAG
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTTATAAGGGGTTAGGGAGCTAT
TTTTGGTTTTGTCTTCACTTTCCTCTGTCTCCTTCTTTATACTTTTCTCAGTTCTAC
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCATAGGGAATCTGGGGGTANCT
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG
GAACTCCTGGACTCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA
GAGGTGAAGAACCGCC

SEQ ID NO: 98_AA498104_M H29974_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCCG
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AAGCTGAGGCCGGCGGCCAGGCCATGGATCCGGCTGGGGCCGAGGTCCCGGGCGAGGCC
TTCTGGCCCGGCGGCCGGATGGCGGCGCGGGGATGTTCTGCACGGCCGCGCTAC
AGCCTCTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTTATGAGGCTGTGGCTGGG
CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG
CAGTTTGAGGAGTGCCTACAGCGCAACGGGTAGCCCAGCGCATGAGTCACGGCAAC
AAGAACTCACAGCTTTACCTGCGCCTGGTGGAGACCTCGCTCAAAGGAGAAAGGATCCTG
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CAGCTTACAAGCGCCATTGCCCTTCCTGCATAAAAACCATCGTGACAGGGACCTAAAG
CCAGACAACATCCTGATCACAGAGCGGTCTGGCACCCCCATCCTCAAGGTGGCAGACTTT
GGACTGAGCAAGGTCTGTGCAGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGATAAC
AAAAATGTGAATGTGAATAAATACTGGCTGTCTCAGCTTGTGGCTCAGACTTCTACATG
GCTCCCGAAGTCTGGGAGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC
CTGGGGACCTACATTAAAGCAAGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCTAGAA
AACCCAAAGATGGAGTTGCATATCCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGGTC

FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA
CTTGAAACCCGAATGGACCAGGTACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG
GGTGTTTTTTAACTAGGTGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA
TGGCAGAGGGTACAGGTGGTGGTGTATCTCCTGACAGCTGGACCTCCCACAATGTGAAGCT
CACGCTTGGGCTGCCCCACTCTACCCTTCTCTTTCTCCTTCAGTAGAATAATAATTGTTTT
TCTAAACATTAAACCATCAAGACTTCTGAAGAGCAGAAGGCTACACTCTG

SEQ ID NO: 99_AA215311_H

CGRCCGCGCTACGGAAAGCCGGAGGGGGCGGGGCCGTGCGCGTAAGGGGGTGTGTCCGC
GCGCACCACGGGGCGCGCGCCGGCTGCTGACTGGAGGCGGCGGCAGCGGAGGCGCGAGC
TGCCCCGATAATGGCGGCCCTGCAGAGCCCATGAGAGGGAGAAGCGGCAGCGTCTACCCTGA
GAAACCTCGACCTTGAAGATGGTGAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG
GCAGTGAAGAAAATTGATGTACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC
TGGGCACCTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC
CTACAAAAGGATGGGATGGTGCAAAGATGTCCCACGGCTCTAATTCTTCCCTTTATTTA
CAGCTTGTAGAACTTCATTAAGGAGAAAATGCTTTGATCCCAGAAGCGCCTATTAT
TTGTGGTTTTGTGATGGATTTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG
AAGCCCAATCGTAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC
TTGCATAAAAACCAGATCATCCACCGAGATCTTAAGCCTGATAACATCCTGATTTCTCAA
ACCAGTTGGATACCAGTGACTTGGAACTACCCTCAAAGTGGCTGATTTTGGTCTAAGT
AAAGTTTGTTCAGCCTCTGGGCAGAACCCAGAAGAACCTGTCAGTGTAAACAAGTGTTC
CTTTCCACAGCATGTGGAACAGATTTTTTACATGGCTCCTGAAGTTTGGGAAGGACATTAC
ACAGCAAAGCTGACATCTTTGCTCTGGGGATTATCATCTGGGCAATGCTGGAAAGGATC
ACATTCATAGACACAGAGACAAAGAAGGAACTCTTGGGGAGTTATGTAAACAAGGAACT
GAGATTGTGCCTGTTGGGGAGGCACTTCTGGAAAATCCCAAAATGGAACCTCTCATTCTC
GTGAAGAAAAATCTATGAATGGGCGAATGAAACAACCTGATTAAGGAAATGCTGGCTGCA
AACCCTCAGGATCGTCCAGATGCTTTTGAAGTAGAAGTACAGATTAGTACAAATTGCATTT
AAAGATAGCAGCTGGGAAACGTGACACATATTATTTGCAAATACCATGGATGATATGCTG
CTTCTGTTTAAACAGTGATGCAACATTATGTGGCTGAAAAAGAATATAAAAAGCTAGACTC
TACCCTCTAAGGGTTTAGATTTTTTTGTGGGATTTTTTTTTTCTCATTCTTAAATCC
AAGTTGGCCGTTTTATTAGTATGTTTCAAATGTGTATTACCAATGTGGGTGTAAATTTTT
AAAAATGATTATTGATAGAAGTTTGGCAGGAAAATTCTTTAAGAGCTAACAAGAGAAGA
GAGTCCAGTTTTCTGGAAATATGTCTTTAAGTATTTTAGACATTCCTCGTCAGTATTAGG
AATTTCCATGGGAAAAGAGTTTGCATGCTGGTAATGCAACCTTTGAACTTTGTAAAGG
AAACATATATGTATATATTTATGTATATGTAAATGTGAATGTGCGCATTTTGCATTCC
ATATGAAAAAATGCCACGTCTGTTTAAATTTATTTGATGTAGTTTGGGTTTTTGAGATT
TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCCTACTCTGCCCCCTCCC
CCTAATGAAATCATATTAAGTNGTTTTTCTNNTTTTTTTTTGTAAATATACAGCTTTTTTTTT
TAAGGCATCATTTTCGAGGGTCTAAATTTATCTGGTAAACAAATGAAATTAAGTGATCC
AAAGCTGCTGAAGTATGTTTGAAGTCTCCAGTGCCCTATAGCTGCAAGAGTTGAATTAGT
CATGCAGTCATATGGCAGCAGGTTGGTGATT

SEQ ID NO: 100_AA018361_H

GCGGGGCCCTCCGTATCCCCACGTGGGCCCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG
AGGCCCAGAGACAGGGGAGGGGCGCCGGGAGCCGGGCGGATCCGCGTCCCCGATGCGCGC
TGCAATTTCCGGCGGGGCGGCGCTGGGGGCAGCGTGAGCCACCCAGTGCTCGGCCCCGCC
GCAACCCGCCGAACCGCCGCCCGCAGCGAGGAAGCGCCCGCGGGGCGCAGGCGGCCCGG
AATGGCGGGGCGCGGCTGGGTCCCCCGCGCCTGGACGGCTTCATCCTCACCGAGCGCCT
GGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT
CACGGAGATTGAGATCCTCAAGGGCATTTCGACATCCCCACATTGTGCAGCTGAAAGACTT
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC
TCGCTTCATCCATAACCCGAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA
ATTAGCTAGCGCCCTGCAATTCCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC
ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAACTGGCAGACTTTGGTTT
CGCACAAACACATGTCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT
GGCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCGCGGTGGACCTCTGGTCCATGGG
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTCGTTCTCGGA
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCTTGCGGCCCTGCTCTC
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTCGCATCTC
CTTCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAG
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATT
AGCAGCCGCCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGCACTA
TGAAGTGGATGCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCG
GGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGAGGCAGGGGAC
CTCTGCCCCGAGACCTGCTCAGAGAGATGGCCCCGGGACAAGCCACGCCTCCTAGCTGCCCT
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGGCCGCCGGCGGGGAGCAGGATGCCCT
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCCGGGCCGG
AGGCGGGAGCTGCTTCACACTGAGGTTTCAAGACCTCATGGCCCCGAGCTGAATACTTGAAG
GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAAGAGGGACTGTCCGAA
TCTGTTCTAGCTCTTGACCCCTTCAGTGACCCTAGAAGAATGATTGGACAGATGTGAGC
CATCTGGAGCAGAGGGGCACTAACCCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG
CCCTGGCGAGCAGGCTTCTTGGATGGACAGTGCTGAGACCCCCATATCCCAGAGTCCCCA
GCCTCCCTCAGGTTACTCTGCACCCCCACAGATGGTTTGTATGGCTGTGCTGTATACTGGAG
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTCATGAGACCTTTGTTACTCGGTGGT
TACTGGGTCTGTGCCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTTGGCTCCGA
GAAGAGGGCAAGGGGCCCCCGCAGGGTACTTCTGTGCTTGCCCTCGCCCTGCCAGCAGGC
AGCTGTGCCCTGGCCTGCCCTTCCCGGGACCCCTTATTCCAACCTCAGCTCCTCTTTGCA
CTGGAATGGGGCACTCCAACACCCCTCAGGGACCACCCTCCCCACAGTATGCACTCAGCC
CCACAGAACCCACCAGTCTTTCTGGGAACCTCACACCTGCCCGCCATCTTGGTACTTTAGG
TTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTTAAAGAGCCCAAGCCTTGTTC
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCTTGGTCTCATCTCTCCACCTCCGTT
CCCTCTGGGCCCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGAGCCTGGGACA
GGGAGAGGGAGGCTTGGAGACAGTCTGACCCAGTGCCCTCTAGGCCACCCACTTCTAGGC
CTGCCCTGCCGCCGTGGAGCCCTGGGCAAGCTCTTTCCCTTTCTGGGCCTGGGTCTCCC
CATCTCTTCAATGGGGCTGATACCTTTCAGACCCACAGCATGGGCACCTTATGAGGACAAA
GTGAATTTAACCTGGAAAAGAATGTATTTGAGAGTTTCTTTTAAATAATCAGCGGGTGT
GGTGATTTGTAGCCCTTCTGCCCTTAAATGCTTCCTTGGGCAAGAGCTGTCTGTCTCTCC
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SEQ ID NO: 101_AA311714_H

TGGACCTGTCCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT
GGACTCTTTTCTTGACTTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATCGTATGTGA
GAAGTCGGCCAGAGATGGAACCTTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTTGTAGCCATTCTTTGTACT
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTCACCCGTGAAATAAACAC
AAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT
GAAAACCTCCCAGAAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGATTACAT
CATCTTCATAAACTTGGCATTCTCTTTTGTGACATTTCTCCTAGGAAGATACTCTTGAA

FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTGTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGTGATAATGGGGAAAATGTC
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT
GAAATGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAGTGTTTCAGAATTAAGTGAAGAG
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCCTAAAGCTTCT
TCAGATTTTATTAATTGCTTGATGGGTACTTCAAAGAGATCCTCAGAAAAGATTGACT
TGGACAAGGCTACTGCAGCATTCAATTTTGAAGAAAAGCTTTTGCTGGAGCAGATCAGGAA
TCAAGCGTCGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTTCTGGGCCACAAGAT
TCCAAGGAGCTTTTGCAGAACTCTCAGAGTAGACAAGCAAAAGGGCACAAGAGTGGTCAA
CCACTAGGTCACTCTTTCAGACTAGAAAATCCAAGTGAAGTTTCGGCCTAAGAGTACTCTT
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCCTACTCCCAGAACTAGC
ACTGCAGTGGAAAGTAAGTCTGGTGAGGATATGACTCACTGTTCAACACAGAAGACTTCT
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGA
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ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCAAGTG
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTCGCAACAAGTGTGCTCG
CAGATCGACTCCACTGAGAAGAGCATGGGGGCTCCCGAGCCAAGCTGAATCTCCTTTGC
TATTTGTGCGTGGTGGCTGGTCACCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTG
TTCCAATTGCTAATCCAGCATTGCGGATAGCTCCAACTGGGATATACGGGCCAAGGTT
GCTCACGTGATTGGTTTACTGGCTTCGCACAACTGAGCTCCAGGAAAATACACCTGTT
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCAACTCCACT
CCAGTGCCTAGACAGTGCCTTGTGTATGTATAGATACTGACAAATATTTCAAATAAATA
AAACTGTATCAGCATT

SEQ ID NO: 102_SGK384_H

TCTTTGGCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC
CTGCGGGGCTGGTCAGCGGCTGCGCTACCTGCACCAGCGGTGCATCCTGCACCGC

SEQ ID NO: 103_AA210451_M SGK384_M

GGTCTGCTGCATGGATAATGGACTGGAACACAGAAAGACCATGCAGGGTTTCGGCTGTAGA
AGGCCAGTATCTCCAGAGGCCAGAAGACACCATCAGATCTCCTGGGACTGGAGTTATAGA
GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA
AACCCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCGGGGCGTGGGGCTGCTGCTCGCCATGG
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCTGGACGAT
CCACCGCGGACTCTAGGCGCTGTCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT
GCTCACGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT
CCCGGCTCACCAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTC
TCACCGAATATCACCCCTTAGGTTCTTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTACAGCA
TCATTAAGTATCTGCATCACAGCCCCCTGGGCACGAGGGTCATGTGTGACTCTAACGACC
TGCCCAAAACATTGTCCAGTACCTGCTAACAAGTAACCTCAGCATTGTGGCAAACGACC
TGGACGCTCTGCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT
TCCAAGACGATCTCATGCCTTCCTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG
TCTCCAGTTTCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTTG
ATATCCATAAGGCGTGCAAGAGCCAGATCCCCGCAGAAAGACCCACTGCTCAGAACGTGC

FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTCGCAGACGAAAG
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTTCAGCC
ACGTAGGCCTCCTCTACGTCTGCCTGCATGTTTGAGTGTTCTGCTCTCCTGGCAGCCCGG
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG
ATTCTGGATCTGCATAGTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC
TGCTTGGTAACTTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGAC
AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTAGAAAGCCCTGTTGGAAGCTGGG
GATGTTTTAACTCCGTGGCAGGGCACTTGCTTAGTTGTGTGCAAAGCCTTGGATCTGACC
CATGGCATGTGCACACACACAAATGCTCAAAGAAAATCCCAGACGCCAGAAAGTGTGCCCC
TTTCTTGTCAATAAGGTCATTGTTCAGTACCGGAGATGATTTTTTTTATGAAGCGTTTATG
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTCTTCTTT
CTTTCTACCCTACTTCTTCCCTTTCCACCCCTAACACTAGATAGGAGAGAGGAGAGAGA
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTCGAGT
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTTCTTCTTGTCTTCTTCTCGCC
CACGACCCTTCAAAACACCGACCAACAGCAAACAACAACCCACCCCGCTTCTCGGGGG
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATTCATATCATCACACTCAGAG
AAACTGTCTGCTGCTGGCAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCACACCTGAGATTAAACAAAAACATT
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG
AGATTGTGGCTGTCTAGAGATTTTTGGAACAGCAAGTTGAAGGAACCTTTCTTACCTGCCT
TGAATGGTGTCTTGAACCTTCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAA
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG
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SEQ ID NO: 104_SGK071_2_H

GAGGTGGTGGCTGTGCAGATGATGGTGGAAATGCATGGATGACCATTACGCCAGTCAGGCC
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CTGTTTCATCACGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGTGAGGTTT
AATGAGCTCAGCTTCCAGGAGGTCAATTGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC
TCTGAGTGGATGCAGAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT
TTGGACATCATCCACAGGAATCTCAAACCCCTCCAACATCATCCTCATCAGCAGTGACCAC
TGCAAACCTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT
CGTGCGGAGGAAGACCCCTTTTCGTAAGTCTGGATGGCCCCCTGAAGCCCTCAACTTCTCC
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC
TCCTTCATGGATGGCACAGAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCAGGC
AGCCTGAAGGCCGTCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC
AGGAATCTTCTGCCCTTGATGCTCCAGATCGACCCCTCGGATCGAATAACGATAAAGGAC
GTTGTGCACATCACCTTCTTGAGAGGCTCCTTCAAGTCTCGTGCCTCTCTTGACCCTG
CACCGGCAGATGGTGCCTGCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC
ATTTTAGGTGATGCTGGGGACACAAAGGGGGAGCGTGCCCTGAAGCTCCTGTCCATGGCC
TTGGCATCCTATTGTTTAGTTCCAGAGGGTTCATTATTTATGCCCTTGGCCTTGCTCCAC
ATGCACGACCAGTGGCTCAGCTGTGACGAGACAGAGTCCCTGGGAAGAGAGACTTTGCC
TCCCTGGGGAACCTAGGGAAGCTGTTGGGCCCCATCCCAAAGGTCTGCCGTGGCCCCCG
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCCCTCGATGTCCAG
CTGTGTGCCTGCTCCCTGCTGCTGACCTCCTGGGCCAAGCGCTGGTGCACACCCCGGAA
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCTGCTGAGTGCTCTTCAGAGCCAC
CCCGAGGAGGAGCCACTTCTTGTTCATGGTCTACAGCCTGCTAGCCATCACCAACCCAG

FIGURE 2BBBB

GAGTCAGAGTCACTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA
AACCACGGAAGCCCGGGAACCCAAGAACCCTGCCAGCACCCAAAGTATCATTGTGAAC
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG
TCAGAGCTGGCGGCCTTCAAGGTGGTGGTGCAGGAGGAGGGCGGCAGTGGCCTCAGCCTC
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG
CTGCTGGTCCACCTGGCTTCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTACCTCCAGCCTGGTGAAGTACAGCAGC
GCCTTCAGCAAACCAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT
GGGGGACTGGAATAG

SEQ ID NO: 105_AA118352_M SGK071_M

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TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT
TAGGCAGCTGGCTGTGTGCTTCTTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG
GCTCGCAGAGACTTGGGTTTGATTTTCAGTCAGTCTCTTGGACAGAGCACCTCTGAAAG
ATGTCATGCAGAATTTCTCCAGTCGACCAGAGGTCCAGCTCAGAGCCATTAACAAGTTGT
TGACAATGCCAGAGGACCAGCTAGGGCTGCCATGGCCACAGAGCTGCTGGAAGAGGTGA
TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC
TGCTGCGTGTTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA
GTTTGATCATCTCCTTCCTGATGGATACCTTGCGGAGCCATCCTAACTCTGAAAGGCTTG
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCTGGAGCACTTCCAAGAGGACA
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTACCTGGGTGCTGGCTACTCATC
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTGG
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA
AGGTGTCCGAACCTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCCTGAGGTGGTGGAGAACCTCT
GCATGCTGTTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCTCTTCAGGC
CCTGACATGCTGCCCTTCTGGTCCGTGGAAGAGAAAGTATCACTAGGTCCAGTATTAA
TTTCGTACCCCATGGTGACTAATAAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106_018653.9_H

GGCCGGGGTCGGGGCGCGGGGCATGCGCGGGCTGGGCAGGGGGCCGGCGGGGCGCAGA
GCGGAGCCGCTCGGAGCCTGAGCCGCCCGGGGCGGGGCGGGGAGCCGCGCGGGGCGG
GCCGGCCGGGGGAGGGGAGCGATGCGGCGCCGCGGGCGGCAGTGGCCGCGGGTTTCTG

FIGURE 2CCCC

CGCCTCCTTCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTCCGAGCCTCCG
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTGCGGGGGCCGC
GGGGAGCTGGCCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG
GGCCCCGGGCCCCGGGCGGGCCGGCCGGAGCGGCGCGCCTGATGGACCTGGCTCCGGGC
GGGCCCCGGCCTGCCGCGCCCCCGGCCCCCTTGGGCCCCGGCCCTGTCCGACGGCGCCCCA
GGCTGGCCCCCGGCTCCCGGCCAGGCTCCCCGGCCCCGGGCCCCGCGCCTGGGCTGCGCC
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC
CGGGTCCGCTGCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC
GATCTGGGCAGCTGCGTGCGGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAG
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCAGACACCCTGACCACCATCAGC
GAGCTGGGCGCCCCCTGTAGAAATGATCCAGCTGCTGCAAACCTTCTGGGAGGATCGATT
CGAATCTGCCTGAGCCTGGGCGCCTCCTCCACCACCTGGCCCACTCCCCACTGGGCTCC
GTCACTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA
CTCGAGTTTCCGGCCAGGAACCTTACCCTGCCCTGCTCAGCCCAGGGCTGGTGGCAGGGC
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTACATACCTCCTGCCT
CACAGTGCCCCGCCTTCACTGCGTCCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG
CTCGCCTGGGGGTGGACGAGACCCTGGCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCA
GACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC
CTCCTTTTCACTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGT
CGGGCCTTTGTGGTCAACCAACCAGACCACCTGGACAGGTCGGCAGCTGGTCTTTTCAAG
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCCTCTGGC
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCTGTG
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AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAT
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT
GACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC
TGTGCCCCCTCCCTGGGACGGTTCCGTGGGCGAGCCCCATCACTGTGTTCAATAGTGTGAGA
ATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGCTGCG
TGGGGACAATCCATCGTGGAGTGTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG
GGGACACTCCCAGGCCAGCCCAGGGGTGAGGGGAGAGGTGCACACCTCAGCATGAGCCA
AGACTGGGGTCAAGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG
GGCCTTTCTGCCTCATTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC
CCCTTCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTGTTAAATTGTTTAT
TTTTGTAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACCTCTTCCC
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SEQ ID NO: 107_AA396601_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGTCTGGCGCGCAGTACGTGGGCTCAG
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CAGTGGACTTCAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCGGGGCGCGAAGGG
GCTGCTATCGCCTGGCGGCCCAAGCTGCTCAAAGAGATGGTGCTGCTGGAGCGGCTGC
GGCACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCAG
ACACGCTGACCACCATCACAGAGCTGGGTGCCCTGTGGAGATGATCCAGCTGTTGCAGA
CTTCTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCTCCTCCACCACCTGG
CCCACTCCCCGCTGGGCTCGGTACCCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACCTTCAGCCTGCCCTGCTCGG
CCCAGGGCTGGTGCGAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT
TCTTACATACCTCCTGCCACACAGTGCCCCGCCCTCCCTCCGACCTCTCCTGGATAGCA
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCCAGCTGGAGA
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG
AGTACCAGCGCATCCCGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG
AGAGCCATGCTCAGTGTCTGTCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGA
AGCTGGTCTTTTTTAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT
ATGTGAAGGCCCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCTGTG
CAGGCGTGACTTGTCATCCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA
CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAATGTGAGTTTGCCAGC
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG
CTCAGGCTGGTCTTAACTGGGACAGTCCCGTGGGCAGCCATTACTGCATTTCATGCTTTG
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG
CCTCATTTGCTTTTCACTGAAAGCCAGGGAGCAGCCGCAGCCAGGCTCCTCCCCTCCTGG
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC
CAGAAGCTTTTATACTTCTCGTTCAATAATTGTTTATTTTGTAAAAAAAATTAAT
CAATTAATAAAATGATGTTTTGTGAC

SEQ ID NO: 108_VRK3_H

ATGATCTCCTTCTGTCCAGACTGTGGCAAAAGTATCCAAGCGGCATTCAAATTCTGCCCC
TACTGTGGAAATTCTTTGCCTGTAGAGGAGCATGTAGGGTCCCAGACCTTTGTCAATCCA
CATGTGTTCATCCTTCCAAGGCTCAAAGAGAGGGCTGAACTCCAGTTTTGAAACCTCTCCT
AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCTCTGAGAGATCCAAAGGCTCCGGGAGC
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCCACAGGGACAGTGCTGACAGAC
AAGAGTGGGCGACAGTGGAAGCTGAAGTCTTCCAGACCAGGGACAACCAGGGCATTCTC
TATGAAGCTGCACCCACCTCCACCTCAGCTGTGACTCAGGACCACAGAAGCAAAAGTTC
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG
GCCGCCAAGCCTCTGCAAGTCAACAAGTGAAGAAGCTGTACTCGACCCCACTGCTGGCC
ATCCCTACCTGCATGGGTTTCGGTGTTCACCAGGACAAATACAGGTTCTTGGTGTTACCC
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTGAGCCCAAAGCATGTGCTGTCAGAG
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCCTCCATGAGAAT
GAGTATGTTTCATGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAAACAGTG
GCCTACGTGGAAGGCAGCAGGAGCCCTCAGCAGGGGGACCTTGAGTTCATTAGCATGGAC
CTGCACAAGGGATGCGGGCCCTCCCGCCGACGACCTCCAGAGCCTGGGCTACTGCATG
CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATTGCCTTCCCAACACTGAGGACATC
ATGAAGCAAAAACAGAAGTTTGTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTAC
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCACGTAT
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG
CGTGTGTCTCCATATGACCCCATTTGGCCTCCCGATGGTGCCCTAG

FIGURE 2EEEE

SEQ ID NO: 109_S71575_M VRK3_M

CCATCCCCACCTGTATCGGCTTTGGCATTACCCAGGACAAGTACAGGTTCCCTAGTATTCC
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG
AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA
ATGAGTATGTTACGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA
GCCAGGTGACCCTGGTGGGCTATGGCTTCACCTACCGATACTGCCCAGGTGGCAAACAG
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG
ACCTGCACAAGGGATGCGGACCCTCCCGCCGAGCGATCTCCAGACCTTGGGCTACTGTA
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGATGGCCCTCAATT
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA
TGCGGGTGTCAACCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG
CTTCCGACTTGACGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAAC
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA
TCAGCACTTGTGTGGGGAACCTGAGTCATGTGTAATGTGAACTCCTCCCTGTCTC
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGCAGCAGCCAC
TCCACTCCCTATGGCATTCTGTGATGGCATAATAAACTGTTTTTAATC

SEQ ID NO: 110_AA45427_H

ATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAACTGTCATCATTGACAATAAGCGCTAC
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CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTACGAGCAGCAGGACCGGGAG
GAGGCCAGCAGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG
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GCCAAGGGTTATGCCACAGAGACTTGAAGCCCAACATATATTGCTTGGAGATGAGGGG
CAGCCAGTTTTAATGGACTTGGGTTCCATGAATCAAGCATGCATCCATGTGGAGGGCTCC
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCCAGCGGTGCACCATCTCCTACCGAGCC
CCAGAGCTCTTCTGTGTCAGAGTCACTGTGTGTCATCGATGAGCGGACTGATGTCTGGTCC
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTCCTAA
AAGGGTGACAGTGTGGCCCTTGCTGTGTCAGAACCAACTCAGCATCCCACAAAGCCCCAGG
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT
CCTCACATTCTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCCAGCTCCTGGCCAA
CATACTACCCAAATCTGA

SEQ ID NO: 111_H05721_H

CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGGACGCCGGTGGTGGCGGCAGC
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CGGCCTGCAGCTGGGTGCGAGCGTCTGCTGCGCTTCACGGGCAAGCCCGGGCGGCTTA
CGGCTTGGGGCGGCGGGCCCGCGGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTCCGGCTCGGGCTCCCTAACCGTCTCCGCTT
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGCAGTTCGTGGTGGCGGC
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CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGAGATCCA
GGCAATTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA
GGGCTTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGCTGC
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACCGG
GTTGCTTCCAGGGAGAGGCCAGGTACAGTGACACAGGAGAAGGGCAGGAGCGAGCTCC

FIGURE 2FFFF

GGGGGCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCCCTC
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCTT
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC
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AGGGGCCCCTGGTCGACTACCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG
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TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT
TGTGGAGCTGGACCCAGACGGCTGCCCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCCT
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGCGG
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCCGTCTGGCCCCAGGGCAGTGAT
TGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCT
TGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGCAGCTACCAAGAGGC
TCAGCTACCTGCAGTCCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT
GCTCCAGCGAGAGGGCCAGCAAGAGACCATCTGCCCGAGTAGCCGCAAATGTGCTTCATCT
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG
CTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGCTCACAGAGAAGTGTTG
TGTGGAACAATAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTAACCGCTCTGCCA
GGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT
GAATTACTAAAAGAACATGGCATCCTCTGTGTCTGATGGTCTGTGAATGGTGAGGGTGG
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGAAAAGGCCTCGGGCTTGG
CAAATGGAAGAACTTGAGTGAGAGTTTCAGTCTGCAGTCCTCTGCTCACAGACATCTGAAA
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAGTTTGGCTGTGACCTTT
GCCCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG
GATGAAGGCAGACATCAACATGGGTGAGCAGTTCAGTTACGGGAGTGGGAAATTACATG
AGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTGGGGATTTAAACTTGAG
GGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAAATGCAATTTACA
ACTGCAGATGACGTATGTGCCTTGAACCTGAATATTTGGCTTTAAGAATGATTCTTCTTAT
ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAGAGATTTTCATGTC
TAACTAACTAACTTTATACATGATTTTTAGGAAGCTATTGCCTAAATCAGCGTCAACATG
CAGTAAAGGTTGTCTTCAACTGACAAA

SEQ ID NO: 112_AI086865_H

AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG
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CAGATGACCAAGGAAGAGCGGCAGGCAGCCAGAATGAGTGCCAGGTCCTCAAGCTGCTC
AACCACCCCAATGTCATTGAGTACTACGAGAAGTTCCTGGAAGACAAAGCCCTTATGATC
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTTCATCCAAAAGCGCTGTAATTCC
CTGCTGGAGGAGGAGACCATCCTGCACCTTCTTCGTGCAGATCCTGCTTGCACTGCATCAT
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA
CACCGCATGGTCGTCAAGATCGGTGATTTCCGCATCTCCAAGATCCTTAGCAGCAAGAGC
ACCCCATGCTATATCTCCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAGAGTGAC
ATCTGGGCCCTGGGCTGTGTCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTTCGAGGCT
GCGAACTTGCCAGCACTGGTGCTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCTGAGTCTACTCAGCCTGGAGCCTGCCAG
CGGCCACCACTCAGCCACATCATGGCACAGCCCCCTCTGCATCCGTGCCCTCCTCAACCTC
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACCAAGTGT
CCGCTGCAGAGAGGCATCATCATGACATTCCGCAGCGGCAGCAATGGGTGCCTAGGCCAT

FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCACCATTTGTGGAGGCTTTGTTGGGCTATGAAATG
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACACTACTAGGCTCTGCACCCCTGGACCAG
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC
AAGTGTGCTGGAGACACAAGCAGTGCCTGGGCACATCATCTACCCTTTTCGCTCTGAC
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCCTGCAACTGTAATTCTAGGCTG
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGCGCGGGCCCAACCTGCTCCCATGTC
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT
GGCTGGTGCAAAAGCTACAGACCTGTCTCTGTGGCAGTGATCCACCATCCACTCTACCAT
GAGTGTGGGGCAGATGATCTAAATGXXAAGAAGAGGAAGAGGAGGAGGAGGAAAAGCAAG
CCCCCATCCCACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACCAGCATG
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAAGCCAAGAAAGGCCAGTTG
ACTAAGAAGAAAAGCCCGGTTAAATTGGAGCCTTCCCCGCCAGACGTGAGCCGATCATT
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCAGAAAGCCGGGAAGAGCTGGAG
AGCGAGGACAGTTACAATGGCCGGGGGAGGAGAACTGTCCAGCGAGGATATTGTGGAA
TCATCATCGCCAGGAAGAGAGAGAAACACAGTCCAGGCCAAAAAGACAGGGGGCAAAGCCC
TCACAAGCCAGGAAGGTAAACAAGAGAAAATCTCCCCAGGATCAAACCCCAACCTCAGT
TGAGGCCAGGTGGTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGGGGGCAAGGGGTGGGCTCAGGGCTG
CAGGGGTTTCTCAAAGGCAATCCAGCTTTCACAAAGGAAGCCCATGGGAAGGCAGGTGGG
AGGGAAAGGAAGGGGCACAGCCCTATTTCTTCTTACCTGCTAGGACAAGGTGGAAGAGTG
TATCTGGGGTGGGAAGGAGGGCTTCCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT
CCACTTCTGGGACAGGCAGTACTGTCTGCAGCGATACCCCAATAAACGGAACCTTTTAA
CCC

SEQ ID NO: 113_AA836348_H

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GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGCACCGAGGATGACTCACTGGTTGTGTGG
AAGGAAGTCGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA
GTTATTCTGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC
CTTCGTCAGAAGGACAAGTTGTTTGAGGAAGAGATGGTGGTGTGGTACCTATTTAGATT
GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA
AATATTTTTCTGACCAAGGCAAACCTGATAAACTTGGAGATTATGGCCTAGCAAAGAAA
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCATATTACATGTCTCCA
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT
GTGAAGATCGTGCAAGGAATTCGGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA
TTGATCCAAAATGGTTCATTTCGTGCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT
GAACTTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA
CCCATTTGCTGTAGTAACATCACGAACAGTGAAGTCTATGTTTGGGGTGGTGGAAAATCC
ACCCCCAGAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG
AATACCCACTTTGCTGTGGTCACAGTGGAGAAGGAAGTGTACACTTGGGTGAACATGCAA
GGAGGCACTAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA
AAGCATGTGGAAAAGTTGCAAGGCAAAGCTATCCGTCAGGTGTCATGTGGTGATGATTTT

FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACTTCTTC
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA
AACAAGGAAGTCTATTCTTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTGAGAA
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGCATGTCGGGAATTATCAACCATGAA
GCATACCATGAAGTTCCCTACACAACGTCTTTACCTTGGCCAAACAGTTGTCTTTTAT
AAGATCCGTACCATTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG
CTGCTGACCTTTGGCTGCAACAAGTGTTGGGCAGCTGGGCGTTGGGAACAACAAGCGT
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT
TCCAATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAACTCCTGACCCA
AGTGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAATCAGTCCC
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCTTGGCTGGCTTCGAAAG
GAGCTGGAAAATGCAGAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGCAGCG
TTTTTCAGAATCTGAGAAAGATACCCTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAACTGAGCTTTTTGCC
TTTGAATCACAACCTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

SEQ ID NO: 114_R86668_H, MKK6_H

ATGAACTTGCTGCTCTCCTACCGCATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG
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TACACTTTTGCCCTCAACCGGAGGAACAGGCCTGGGGACCGGGCGAAGGCCCTGTCTGTG
CTGCTGCCGCTGGTACAGCTTGAGGGCTCTGTGGCGCCCGATCTGTACTGCATGTGTGGC
CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCCAGCCTTCACTCAGGCATCAAT
GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAAGAGCTCCGGCTA
ATAGGCATGAAGCTGGGCTGCCTGCTGGCCCGCAAAGGCTGCGTGGAGAAGATGCAGTAT
TACTGGGATGTGGGTTTCTACCTGGGAGCCAGATCCTCGCCAATGACCCACCCAGGTG
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCCATATGGTACCTGGTGTCCTGT
ATGGAGACCTTCTGCTCTACCAGCACTTCAGGCCCACGCCAGAGCCCCCTGGAGGGCCA
CCACGCCGTGCCCACTTCTGGCTCCACTTCTTGCTACAGTCTTGCCAACCATTCAGACA
GCCTGTGCCAGGGCGACCAAGTGCTTGGTGCTGGTCTTGAGATGAACAAGGTGCTGCTG
CCTGCAAAGCTCGAGGTTTCGGGGTACTGACCCAGTAAGCACAGTGACCCTGAGCCTGCTG
GAGCCTGAGACCCAGGACATTCCCTCCAGCTGGACCTTCCCAGTCGCCTCCATATGCGGA
GTCAGCGCCTCAAAGCGCGACGAGCGCTGCTGCTTCTCTATGCACTCCCCCGGCTCAG
GACGTCCAGCTGTGCTTCCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG
GCCTGGGTGACGAACCCGATTCACGCGCGCCGCGGAGGAGCGGAGGGCGCGGGGGAG
ATGTTGGAGTTTGATTATGAGTACACGGAGACGGGCGAGCGGCTGGTGCTGGGCAAGGGC
ACGTATGGGGTGGTGACGCGGGCCGCGATCGCCACACGAGGGTGCGCATCGCCATCAAG
GAGATCCCGGAGCGGGACAGCAGGTTCTCTCAGCCCCTGCATGAAGAGATCGCTCTTCAC
AGACGCCTGCGCCACAAGAACATAGTGCGCTATCTGGGCTCAGCTAGCCAGGGCGGGTAC
CTTAAGATCTTCATGGAGGAAGTGCTGGAGGCAGCCTGTCTCCTTGTGCTGCGTCCGGTG
TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG
GGACTTGGCTACTTGCACGACAACCACATCGTGACAGGGACATAAAAGGGGACAATGTG
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG
GCAGGCATCACACCTTGCACTGAGACCTTCACAGGAACTCTGCAGTATATGGCCCCAGAA

FIGURE 2III

ATCATTGACCAGGGCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC
ACTGTCAATTGAGATGGCCACAGGTGCCCCCCTTCCACGAGCTCGGGAGCCACAGGCT
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCAGCTCTCTGTGCGCC
GAGGCCCAAGCCTTTCTCCTCCGAACCTTTTGAGCCAGACCCCCGCCTCCGAGCCAGCGCC
CAGACACTGCTGGGGGACCCCTTCTCGCAGCCTGGGAAAAGGAGCCGAGCCCCAGCTCC
CCACGACATGCTCCACGGCCCTCAGATGCCCCCTTCTGCCAGTCCCACTCCTTCAGCCAAC
TCAACCACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCCTCTCAGCACCCACCCAGC
CCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCCGAGGAGCCT
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTGCGGGCTGAGCCTGCTGCACCAGGAG
AGCAAGCGTCGGGCCATGCTGGCCGAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG
AATCTGCACCAGGAGCAGAAGCAAGAGCAGGGGGCCCGTCTGGGCAGAAACCATGTGGAA
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGGCAGCTCGCCCAG
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGCCAGGGCCTTGGGCCTGCGCTTCTGCAC
AGACCGCTGTTTGCCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT
CCACACTGGATGTTCTGTTCTGGAATCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT
GTGCTAGGACCGGAGGTGGAGAAGGAGGCGGTCTCACCGAGGTCAGAGGAGCTGAGTAAT
GAAGGGGACTCCAGCAGAGCCCAGGCCAGCAGAGCCCCGCTTCCGGTGAGCCCCGAGCAG
GGCCCCGCTCCTCTGATGGTGAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGACGCGGGCTCTACAGCGG
CTGAATGAGGAAGCCCGGACCTATGTCCTGGCCCCAGAGCCTCCAAGTCTCTTTCAACG
GACCAGGGCCTGCTGAGTGGCTACAGGAAGTGAATGTGGATTACAGGCACCATCCAAATG
CTGTTGAACCATAGCTTACCCCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

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CCCATCCAGCTGGCTCCTATGAAGACAATCGTTAGAGGAAACAAACCCTGCAAGGAAACC
TCCATCAACGGCCTGCTAGAGGATTTTGACAACATCTCGGTGACTCGCTCCAACCTCCCTA
AGGAAAGAAAGCCCACCCACCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG
GAAGAAAATGGCTTCATCACCTTCTCCAGTATTCCAGCGAATCCGATACTACTGCTGAC
TACACGACCGAAAAGTACAGGGAGAAGAGTCTCTATGGAGATGATCTGGATCCGTATTAT
AGAGGCAGCCACGCAGCCAAGCAAAATGGGCACGTAATGAAAATGAAGCACGGGGAGGCC
TACTATTCTGAGGTGAAGCCTTTGAAATCCGATTTTGCCAGATTTTCTGCCGATTATCAC
TCACATTTGGACTCACTGAGCAAACCAAGTGAATACAGTGACCTCAAGTGGGAGTATCAG
AGAGCCTCGAGTAGCTCCCCTCTGGATTATTCAATCCAATTCACACCTTCTAGAAGTGA
GGGACCAGCGGGTGCTCCAAGGAGAGCCTGGCGTACAGTGAAAGTGAATGGGGACCCAGC
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ACCATGCGGCAGAGGTCCAGGTGAGGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA
GCAAGTGCAATTTAAAACCCATCCCCAAGGACACTCCTACAACCTCTACACCTACCCTCGC
TTGTCCGAGCCCACAATGTGCATTCCAAGGTGGATTACGATCGAGCACAGATGGTCCTC
AGCCCTCCACTGTCAGGGTCTGACACCTACCCAGGGGCCCTGCCAACTACCTCAAAGT
CAAAGCAAATCGGGCTATTCTCAAGCAGTCACCAGTACCCGTCTGGGTACCACAAAGCC
ACCTTGTAACCATACCCCTCCCTGCAGAGCAGTTCGAGTACATCTCCACGGCTTCTTAC
CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCAGCTGGGGCTCCTCCTCC
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGGCCCTGCAGCTGGTGGTC
AGCCCAGGAGACCCAGGGAATACTTGGCCAACCTTTATCAAAATCGGGGAAGGCTCAACC
GGCATCGTATGCATCGCCACCGAGAAACACACAGGGAAACAAGTTGCAGTGAAGAAAATG

FIGURE 2JJJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT
TACCACCATGACAAATGTGGTTGACATGTACAGCAGCTACCTTGTGCGCGATGAGCTCTGG
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAT
AACCAAGGAGTGATTACAGGGACATAAAAAGTGAATCCATCCTCCTGACAAGCGATGGC
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG
AAATCATTTGGTTGGCACTCCCTACTGGATGGCCCCCTGAGGTGATTTCTAGGCTACCTTAT
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG
CCCCCTACTTCAATGAGCCTCCCCCTCAGGCGATGCGGAGGATCCGGGACAGTTTACCT
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCTAGACTTGATG
TTGGTGAGGGAGCCCTCTCAGAGAGCAACAGCCCAGGAACTCCTCGGACATCCATTCTTA
AAACTAGCAGGTCCACCGTCTTGCATCGTCCCCCTCATGAGACAATACAGGCATCACTGA

SEQ ID NO: 116_SURTK106_H

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AAACTAGGAAGGCAAGGAATGGCAAGGTGAGGAATTACTCACAGCTGTGCTGTGTGCATT
CTCTGTGGGCCTAGCAGGGAAGGGGACAGCCCTGTGGCAATGGGCATGACACGGATGCTC
CTGGAATGCAGTCTCAGTGACAAGTTGTGTGTGCATCCAGGAGAAGCAGTATGAAGTGATT
ATCGTCCCAACTTTGTTGGTTACTATCTTCCTCATCCTTCTTGGGGTCATCCTGTGGCTT
TTTATCAGAGAACAAGAACTCAACAGCAGCGTTCTGGACCTCAAGGCATTGCCCCGTGT
CCTCCACCTAGGGACCTAAGCTGGGAAGCAGGACATGGAGGAAATGTGGCTTTGCCACTT
AAGGAGACATCCGTGGAAAACCTTCTGGGAGCTACCACACCTGCCCTGGCTAAGCTGCAG
GTGCCGCGGGAGCAACTCTCTGAAGTTCTGGAGCAGATTGTCAGTGGTAGCTGTGGGCCC
ATCTTTTCGAGCCAATATGAACACTGGGGACCCTTCTAAGCCCAAGAGTGTTATTCTCAAG
GCTTTAAAGAACCAGCTGGGCTCCATGAGGTACAAGATTTCTTAGGGCGAATCCAATTC
CATCAATACCTGGGGAAACACAAAAACCTGGTGCAGCTGGAAGGCTGCTGCACTGAAAAG
CTGCCACTCTATATGGTGTGGAGGATGTGGCCCAGGGGACCTGCTCGGCTTTCTCTGG
ACCTGTGCGCGGGATGTGATGACTATGGATGGTCTTCTCTATGATCTCACAGAAAAACAA
GTATATCACATCGGAAAGCAAGTCCTTTTGGCGCTGGAATTCCTGCAGGAGAAGCATTG
TTCCATGGGGATGTGGCAGCCAGGAATATTCTGATGCAAAGTGATCTCACTGCTAAGCTC
TGTGGATTAGGCCTGGCTTATGAAGTTTACACCCGAGGGGCCATCTCCTCTACTCAAACC
ATACCTCTCAAGTGGCTTGCCCCAGAACGGCTTCTCCTGAGACCTGCTAGCATCAGAGCA
GATGTCTGGTCTTTTGGGATCCTGCTCTATGAGATGGTGACTCTAGGAGCACCACCGTAT
CCTGAAGTCCCTCCTACCAGCATCCTAGAGCATCTCCAAAGAAGGAAAATCATGAAGAGA
CCCAGTAGCTGCACACATACCATGTACAGTATCATGAAGTCCTGCTGGCGCTGGCGTGAG
GCTGACCGCCCCCTCACCTAGAGAGCTGCGCTTGCGCCTAGAAGCTGCCATTAAAACTGCA
GATGACGAGGCTGTGTTACAAGTACCAGAGTTGGTGGTACCTGAACTGTATGCAGCTGTG
GCCGGCATCAGAGTGGAGAGCCTCTTCTACAACATAGCATGCTTTGAAGAGTCTCGGGC
AAGAAACATTCATGCATGAGTATATGTTCTTGGAAATCAATTCTCTAAGAACAGAGAATG
GTCTTTCCAGGGACACAAAGGGAGAAATGGGACATGGATTCTTGATCTTCCTTTACACA
TTTCTCGGGAAATCTGAAATGATGCTGGATGGGACTCTACACATCCTGAGCTAAGACATA
CTGTCACTCTCACTTCTGCTGTCCAGTCTTAGAAATCCTGGGTAGAAGTGGTGGACCTG
TGCAAGGAGGTTTTAGAACTCTGCAGTATTTGTTGGGGCATGGCACAAATAAGCTCATC
CCTCCCGTCCGAGGCTAGTTTCTCTGGAACACATTTTATCTAGATGAAAATTTGGAA
TGAAATGAAGGAATAGAAATCCAATAAAAGAGTTGAAGGGAAAGAAAATTTAAGGTTCTT
CTTGCTCAGGATTACAGATATGGACCAACACCTCCTTCAAGAAAAGGTGGTAGGACACAA
AGTTCTTCAGTCCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC
TGAGTTTACCTTAGGTATAGATAAAAGAAAGATGGTCCCCTTTTATCTGATTCTGAGAC
AGGTAAATTCTGTTTGTACTACGTTTAATTAGAAGGTGGAGGAGTCATTTTCATGATTAA

FIGURE 2KKKK

GAACATTCAACATGTATTGTTCAATTAAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAAAGAATTCTGTGTGTGTGTGTGTGTGT
GTGTGTGTGTGCACAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA
GTCTTTAACAAGGGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATT
TTCAATCATCTGTTGATATACTGTGAAACTTATTTTATTAAATTAATATTTATTAAATGG

SEQ ID NO: 117_AA098024_M

CTGCAGGAGAAGCACCTGTTTCATGGGGATGTGGCTGCCAGGAACATCCTGATCCAAAGT
GACCTGACTCCCAAACCTTTGTCATCTGGGCCTGGCTTATGAAGTTCATGCCCATGGGGCC
ATCTCCTCTGCTCGATCCAGCACCATCCCTCTCAAGTGGCTTGCTCCAGAAAGGCTTCTC
CTGAGACCTGCAAGCATCAGGGGAGATATTTGGTCCTTTGGGATCCTGCTTTATGAGATG
GTGACTCTAGGAGCACCACCATAACCCTGAAGTCCCTCCCACCAGCATCCTACAATATCTT
CAGAGAAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG
AAGTGCTGTTGGCGCTGGAGTGAGGACAGCCGCCCTTACTTGTTGAGCTGCTCCAGCGC
CTAGAAGCTGCTTCTAGATCTGCCGATGACAAGGCTGTGTTGCAAGTGCCAGAGTTGGTG
GTGCCTGAACTGTATGCAGATGTGGCTGGCATCAGGGCAGAAAGCATTTTCTATAGCTTC
AGTGTCTTTGAAGATGGTCTTAGACAAATGACTATATATGGGTGGAATTAGTTCCTTCA
AGAACAGAGAGAAGGAACTTTCTGTGGCCACCAAGGGAGAAAAAAGGACATGGATCTTG
CATCTTTCCCTAAACATTTTCTTAGACATCTGAAATGCTGCTGGATGAAGCTCTACCTCT
ACATACCATGTACTCTTGAGCTAAGAATCACCATCAATTGTAGTTTGCTTTCCAGTCCCA
AGGGCTGAAGTATAAGTGGTGGACCGTGTCTTCTAAAGGAGGTTTTTAAATCTGCAAT
GATTGTAAGGGAATTAGGCAAAAGGGCTGGTCCCACTCACTCCAGGCTGGTTTACTACTG
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ATGGGCATGAATGAACACCTTCTAATTTTAAACCATGAATTGAATATTGGAATTCATGAG
AAAGAAAATTCTAGGTTCTTTTGTCTAAGAGGTGTTAAGGTGAGTCAATATATCCTTCAA
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GCTGAAGAAGATCTATAAGAAACAATACTGAGCCTTTCTTGACTATAGATAGAAGAGCA
TCCTTTTCATTGAACTCTGAGGCAGGTGGACCATGCATGATACTAAGTTTAAATTAGAAGCA
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GACTAAGGAGAATCAGCCTATAGAGCCAAAGCTAGAACCAGGGATAAAAAGTGTGTGTGT
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AAGAGGTACAGAGAAGAAGTAATCTTATAGGAATGGATGGTAGCTTCTAATTTTAAACCA
TTCATTGAAATAACTGTGAAGCAACTCATTAACTAGTATTTATTGACCAAAAGTAGACT
TTTCAGGTGTATAGCTGCCAAAATCTCTATAATAAGAGGCTAAAAGAAAATAAATGGGA
GTTATTTTACTAGGAAAATTAGAGAACCTATAGTTTCCAAAAAGAGATTCTTTATGTGCA
AAATGAGATAACTCTCTACCTCACAGGGTTGGTGTGAGGAACAATGAGAATATGTATTTG
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SEQ ID NO: 118_SGK2ALPHA_H

GAAGAGGGCAGAGCCGTGCATGGGGCTGCTCCCCAGGACCTGAGCAGGAACCTGGAGTTT
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CAGCCCTCCAGGGCCAATGGGAACATCAACCTGGGGCCTTCAGCCAACCCAAATGCCAG
CCCACGGACTTCGACTTCTCTCAAAGTCATCGGCAAAGGGAACTACGGGAAGGTCTACTG
GCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGTGAAGGTACTACAGAAAAAGTCCATC
TTAAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAACGTG
CGGCACCCCTTCTCGTGGGCCTGCGCTACTCCTTCCAGACACCTGAGAAGCTCTACTTC
GTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCCGGTTC
CTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGTGGCCAGCGCCATTGGCTACCTGCAC
TCCCTCAACATCATTTACAGGGATCTGAAACCAGAGAACATTCTCTTGGAAGTCCAGGGA
CACGTGGTGTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA

FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT
GATCGAGCAGTGGACTGGTGGTGGCTTGGGGGAGTCCCTCTACGAGATGCTCCATGGCCTG
CCGCCCTTCTACAGCCAAGATGTATCCCAGATGTATGAGAACATTCTGCACCAGCCGCTA
CAGATCCCCGGAGGCCGGACAGTGGCCGCTGTGACCTCCTGCAAAGCCTTCTCCACAAG
GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTG
TCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCA
TTCCTGGGATTTTCTTATGCGCCAGAGGATGATGACATCTTGATTGCTAGAAGAGAAGG
ACCTGTGAACTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGCTAGGAA
GAGCGACTCAAACATAAATGGCTTCAACGAGAAGCAGGTTATTTTTTCCAGCACATAA
AAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC
TGATCTCTGCCCCTGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTGCTACAAGATG
GTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGA
GAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAGCTCCCCCAATGACTTTTGCTT
CCATCTCACTAACCACCCACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCTTATTTGC
TGGGTACGTGACTATCCCTAATAACAAAGGGGTTTTGACCCTAAGACATTAGGGGAGAAT
GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTGTTGGATTTTGATCT
CAATGTGTAAATGACAGAGATGTAAACAGCTCATAGGGTATCAATATCTCTTATTGTTT
TATGTTGAAAAA

SEQ ID NO: 120_CCRK_H

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SEQ ID NO: 121_TESK2_H

GAATTCGCGGCCGCTCGACGCTCAGCAGAGCTACCAGCTGCCCTGTTGGCTTCGCTGGT
GGATCGTCTCCTGGCCCCGCCAAACAGGCGAGCGGCCCGACTGTGGGGCATGGCAGTA
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FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC
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TGCTTCTGTTGATTTTTTTTTGTAAACTTTCCCAAGACATTTTCAGACTTAAAAATAA
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